

83844

STIC-Biotech/ChemLib

From: Bugaisky, Gabriele
Sent: Wednesday, January 08, 2003 1:29 PM
To: STIC-Biotech/ChemLib
Subject: 09/943692

please search SEQ ID NO:2 and truncations thereof >530 aa.

thanks, gabi

Gabriele E. Bugaisky
* au 1653
* cml-10d09; mailbox 9b01
* 308-4201

Gabi,
truncations >530 should be
retrieved in the standard search.
However, I thought an oligomer search
might also be helpful, since it provides
a list of seqs that contain ^{areas of} contiguous
100% matches to the query seq. Hits are
listed in decreasing order of the length
of the 100% match region.
Barb

Point of Contact:
Barb O'Brien
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 1-10-03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 10:44:24 ; Search time 39 Seconds
(without alignments)
2200.344 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406
Sequence: 1 NKPNNRSEHDTIKTENNEV.....TGLSAGKRVYIDKIEFIPVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.101002:*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	644	8 AAP70085	Sequence of toxin
2	3406	100.0	644	9 AAP82487	Delta endotoxin en
3	3406	100.0	644	10 AAP94679	Amino acid sequenc
4	3406	100.0	644	10 AAP95595	M-7 crystal toxin.
5	3406	100.0	644	14 AAP939751	Delta endotoxin.
6	3406	100.0	644	15 AAP85697	CryIIIB insecticida
7	3406	100.0	644	15 AAP85698	CryIIIB insecticida
8	3406	100.0	652	20 AAP93214	Amino acid sequenc
9	3403	99.9	644	17 AAP99960	B.t.t. coleopteran
10	3403	99.9	644	18 AAP34817	Novel CryIIIA muta

11	3403	99.9	644	18 AAP34827	Novel CryIIIA muta
12	3403	99.9	644	18 AAP34829	Novel CryIIIA muta
13	3403	99.9	644	18 AAP34841	Novel CryIIIA muta
14	3402	99.9	644	18 AAP34822	Novel CryIIIA muta
15	3402	99.9	644	18 AAP34828	Novel CryIIIA muta
16	3401	99.9	644	18 AAP34812	Novel CryIIIA muta
17	3401	99.9	644	18 AAP34820	Novel CryIIIA muta
18	3401	99.9	644	18 AAP34832	Novel CryIIIA muta
19	3401	99.9	644	18 AAP34834	Novel CryIIIA muta
20	3401	99.9	644	18 AAP34835	Novel CryIIIA muta
21	3401	99.9	644	18 AAP34836	Novel CryIIIA muta
22	3400	99.8	644	18 AAP34813	Novel CryIIIA muta
23	3400	99.8	644	18 AAP34818	Novel CryIIIA muta
24	3400	99.8	644	18 AAP34821	Novel CryIIIA muta
25	3400	99.8	644	18 AAP34825	Novel CryIIIA muta
26	3400	99.8	644	18 AAP34826	Novel CryIIIA muta
27	3400	99.8	644	18 AAP34830	Novel CryIIIA muta
28	3400	99.8	644	18 AAP34840	Novel CryIIIA muta
29	3398	99.8	644	17 AAP99958	Bacillus thuringie
30	3398	99.8	644	17 AAP34814	Novel CryIIIA muta
31	3398	99.8	644	18 AAP34815	Novel CryIIIA muta
32	3398	99.8	644	18 AAP34816	Novel CryIIIA muta
33	3398	99.8	644	18 AAP34823	Novel CryIIIA muta
34	3398	99.8	644	18 AAP34824	Novel CryIIIA muta
35	3398	99.8	644	18 AAP34831	Novel CryIIIA muta
36	3398	99.8	644	18 AAP34833	Novel CryIIIA muta
37	3398	99.8	644	18 AAP34839	Novel CryIIIA muta
38	3397	99.7	644	18 AAP34811	Novel CryIIIA muta
39	3397	99.7	644	18 AAP34837	Novel CryIIIA muta
40	3397	99.7	644	18 AAP34838	Novel CryIIIA muta
41	3386	99.7	644	9 AAP80467	Bacillus thuringie
42	3382	99.6	644	18 AAP34819	Novel CryIIIA muta
43	3329	97.7	644	22 AAP84195	Amino acid sequenc
44	3328	97.7	645	18 AAP34784	An artificial modl
45	3149	92.5	597	17 AAP00334	Bacillus thuringie

ALIGNMENTS

RESULT 1
ID AAP70085 standard; Protein; 644 AA.

XX AAP70085;
AC
XX
XX
DT 04-MAY-1991 (first entry)
XX
DE Sequence of toxin which is toxic to beetles of the order
DE Coleoptera.
XX
KW Microbial pesticide.
XX
OS Bacillus thuringiensis strain san diego.
XX
PN EP213818-A.
XX
PD 11-MAR-1987.
XX
PF 08-AUG-1986; 86EP-0306151.
XX
PR 16-JUN-1986; 86US-0874727.
PR 16-AUG-1985; 85US-0767227.
PA (MYCO-) MYCOGEN CORP.
PI Herrnsstadt C, Wilcox E;
XX
DR WPI; 1987-066492/10.
DR N-PSDB; AAN70092.
XX
PT New poly:peptide toxin having pesticidal activity - formed by
PT bacillus thuringiensis toxin gene, and useful for killing

PF Coleoptera beetles
 XX
 PS Claim 3; pp15-16; 19pp; English.
 CC B. thuringiensis toxin gene toxic to Coleoptera beetles is cloned
 CC and expressed. Live micro-organisms for inhibiting the growth of, or
 CC killing, the beetles are obtd. The polypeptide toxin may be isolated
 CC for use against the beetles.
 XX
 XX Sequence 644 AA;
 SQ
 Query Match 100.0%; Score 3406; DB 8; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPNNRSEHDITKTENNENVPINHOYPLAETPPTLEDLNYKEFLRMTADNTEALDSS 60
 DB 1 MNPNNRSEHDITKTENNENVPINHOYPLAETPPTLEDLNYKEFLRMTADNTEALDSS 60
 QY 61 TTKDVIQKGISVVDLGVGVPFGGALVSEFTNPLNTIMPSEDPWKAFFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVDLGVGVPFGGALVSEFTNPLNTIMPSEDPWKAFFMEQVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNVEDVYSSLSWQKNPVSSRNHSGRIRELSQASHFRNS 180
 DB 121 IADYAKKALAELOGLONNVEDVYSSLSWQKNPVSSRNHSGRIRELSQASHFRNS 180
 QY 181 MPSEFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEYT 240
 DB 181 MPSEFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEYT 240
 QY 241 DHCKKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLDYVRLYPREVTELT 300
 DB 241 DHCKKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLDYVRLYPREVTELT 300
 QY 301 RDVLTDPVGVNNLRGVTGTFNSNENYIRKPHLEFDYLHRIQFHTROPQGYGNDSEFNYS 360
 DB 301 RDVLTDPVGVNNLRGVTGTFNSNENYIRKPHLEFDYLHRIQFHTROPQGYGNDSEFNYS 360
 QY 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 QY 421 KVEESQVNDQDEASTQYDSKRNVAWSIDQLPPEPTTDEPLEKGYSHQNLNYMCEL 480
 DB 421 KVEESQVNDQDEASTQYDSKRNVAWSIDQLPPEPTTDEPLEKGYSHQNLNYMCEL 480
 QY 481 MOGSRGTIPVLTWTHKSVDFENMIDSKITQLPLVAKAYKLGASAVVAGPRFTGGDITL 540
 DB 481 MOGSRGTIPVLTWTHKSVDFENMIDSKITQLPLVAKAYKLGASAVVAGPRFTGGDITL 540
 QY 541 TEMGSAATIVTDPVYSOKYRARIHYASTSQITFTLSLDGAFNOYFEDKTIINKGDTLT 600
 DB 541 TEMGSAATIVTDPVYSOKYRARIHYASTSQITFTLSLDGAFNOYFEDKTIINKGDTLT 600
 QY 601 YNSFNILASFSTPELGGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNILASFSTPELGGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 RESULT 2
 AAB82487
 ID AAB82487 standard; protein; 644 AA.
 AC AAB82487;
 XX
 XX 01-NOV-1990 (first entry)
 DE Delta endotoxin encoded by cryC.
 XX Coleoptera; toxin; cryC; insecticide; delta-endotoxin; Lepidoptera.
 XX Bacillus thuringiensis EG2158.

XX
 FH Key Location/Qualifiers
 FT Reptide 1..53 /label=signal_peptide
 FT Protein /note="6 kD"
 FT 54..644 /label=mature_toxin
 XX
 XX MO8080880-A.
 XX
 PD 17-NOV-1988.
 XX
 PF 04-MAY-1987; 87WO-US01495.
 XX
 PR 06-MAY-1987; 87US-0047945.
 XX
 PA (ECOG-) ECOGEN INC.
 PI Donovan WP, Gonzales JM, Levinson BL, Macaluso A;
 XX
 XX WPI: 1988-338229/47.
 DR N-PSDB; AAN82139.
 XX
 PT New gene encoding delta endotoxin of *Bacillus thuringiensis* -
 effective as insecticide against Coleoptera.
 CC
 PS Claim 10; Fig 8; 82pp; English.
 CC The cryC gene encodes a delta endotoxin which is an insecticide
 CC effective against Coleoptera and Lepidoptera. The sequence was
 CC isolated from cDNA library, on a plasmid designated pEG212. The
 CC plasmid can be used to construct an expression vector which can
 CC be used to transform *B. megaterium* ATCC 35985. Colorado potato
 CC beetle larvae treated with a suspension of cultured cells were
 CC dead within one week. The protein can be used as pure crystals
 CC or in the form of B.t. spores.
 CC See also AAN82141.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 3406; DB 9; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPNNRSEHDITKTENNENVPINHOYPLAETPPTLEDLNYKEFLRMTADNTEALDSS 60
 DB 1 MNPNNRSEHDITKTENNENVPINHOYPLAETPPTLEDLNYKEFLRMTADNTEALDSS 60
 QY 61 TTKDVIQKGISVVDLGVGVPFGGALVSEFTNPLNTIMPSEDPWKAFFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVDLGVGVPFGGALVSEFTNPLNTIMPSEDPWKAFFMEQVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNVEDVYSSLSWQKNPVSSRNHSGRIRELSQASHFRNS 180
 DB 121 IADYAKKALAELOGLONNVEDVYSSLSWQKNPVSSRNHSGRIRELSQASHFRNS 180
 QY 181 MPSEFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEYT 240
 DB 181 MPSEFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEYT 240
 QY 241 DHCKKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLDYVRLYPREVTELT 300
 DB 241 DHCKKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLDYVRLYPREVTELT 300
 QY 301 RDVLTDPVGVNNLRGVTGTFNSNENYIRKPHLEFDYLHRIQFHTROPQGYGNDSEFNYS 360
 DB 301 RDVLTDPVGVNNLRGVTGTFNSNENYIRKPHLEFDYLHRIQFHTROPQGYGNDSEFNYS 360
 QY 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 QY 421 KVEESQVNDQDEASTQYDSKRNVAWSIDQLPPEPTTDEPLEKGYSHQNLNYMCEL 480


```

Db 421 KVEFSQYNDQTDASTQYDTSKRNGAVSWDSIDQLPPTDEPLEKGYSHQINVMCEFL 480
QY 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQLPLVAKYKQSGASVYAGPRFTGGDIIOC 540
Db 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQLPLVAKYKQSGASVYAGPRFTGGDIIOC 540
QY 541 TENGSAATIVTPDVASQYKRYARIHYASTQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
Db 541 TENGSAATIVTPDVASQYKRYARIHYASTQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNILASFSTPELSCNNLQIGVTGLSAGDKYIDKIEFIPVN 644
Db 601 YNSFNILASFSTPELSCNNLQIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 3
AAP94679
ID AAP94679 standard; protein; 644 AA.
AC AAP94679;
XX 17-JUL-1990 (first entry)
XX Amino acid sequence of the Btl3 protein.
XX Bacillus thuringiensis tenebrionis; 66 kDa crystal protein; btl3 gene;
XX Btl3 protein; toxin; Coleoptera; pYVE38.
XX Bacillus thuringiensis.
XX Key Location/Qualifiers
XX FH 58..79
XX FT /note="N-terminal residues of the Btl3 protein"
XX FT Misc-difference 58
XX FT /note="This residue was not unambiguously determined.
XX FT It could possibly be Ser."
XX FT Misc-difference 60
XX FT /note="As above. It could possibly be Pro."
XX FT Misc-difference 64
XX FT /note="As above. It could possibly be Gln."
XX PN W08901515-A.
XX PD 23-FEB-1989.
XX PE 15-AUG-1988; 88WO-EP00752.
XX PR 29-DEC-1987; 87GB-0030261.
XX (PLAN-) PLANT GENETIC SYSTEMS.
XX Vaecck M, Hofte H, Botterman J;
XX WPI: 1989-068871/09.
XX DR N-PSDB; AAN91071.
XX Plant cell transformed with DNA -
XX is for Bacillus thuringiensis toxic protein and is resistant to
XX Coleoptera pests
XX Disclosure; : 35pp; English.
XX The btl3 gene encodes a 66 kDa crystal protein (the Btl3 protein) which
XX is believed to be the active protein in the crystal toxin (the Btl3
XX toxin) produced by Bacillus thuringiensis (B.t.) tenebrionis and B.t.
XX S1. The patent is for a transformed plant cell which includes, inserted
XX in its genome, the btl3 gene, or a fragment which encodes the 66kD
XX crystal protein. Plant cells contg. DNA encoding this protein are
XX protected against Coleoptera. Also new are plants (and their seeds)
XX contg. these cells; a specific DNA sequence of 1760 b; the crystal
XX protein; and microorganisms transformed with the DNA.

```

```

SQ Sequence 644 AA:
Query Match 100.0%; Score 3406; DB 10; Length 644;
Best Local Similarity 100.0%; Pred. No. 1,7e-268;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENVPNNHVOYPLAETPNPTLDDIYNKELRMTAANNTEALDSS 60
Db 1 MNPNNRSEHDITKTENNENVPNNHVOYPLAETPNPTLDDIYNKELRMTAANNTEALDSS 60
QY 61 TTKDVIQKISIVVGDILGVGPFPGALVSFTYNFLNTIMPSEDPMKAFMEQVEALMDOK 120
Db 61 TTKDVIQKISIVVGDILGVGPFPGALVSFTYNFLNTIMPSEDPMKAFMEQVEALMDOK 120
QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQASHFRNS 180
Db 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQASHFRNS 180
QY 181 MPEFAISGVEVLETTYAQAAMTHLFLKDAQIYGEWGEKEDIAPFYKROKLTJOEYT 240
Db 181 MPEFAISGVEVLETTYAQAAMTHLFLKDAQIYGEWGEKEDIAPFYKROKLTJOEYT 240
QY 241 DHCVKMYNGLDKLRSSYESWVNFNRYRREMTLVLDLALFPLDYRLYPREVKTETLT 300
Db 241 DHCVKMYNGLDKLRSSYESWVNFNRYRREMTLVLDLALFPLDYRLYPREVKTETLT 300
QY 301 RDVLTDPVIGVNNLRGYGTFESNIENYIRKPHLFYLRHQFTRRQPGYGNDSFNTWS 360
Db 301 RDVLTDPVIGVNNLRGYGTFESNIENYIRKPHLFYLRHQFTRRQPGYGNDSFNTWS 360
QY 361 GNYVSTRPSIGSNDITTSPEYGNKSEEPVONLEFNEKRYRAVANTNLAVMPSAYISGVT 420
Db 361 GNYVSTRPSIGSNDITTSPEYGNKSEEPVONLEFNEKRYRAVANTNLAVMPSAYISGVT 420
QY 421 KVEFSQYNDQTDASTQYDTSKRNGAVSWDSIDQLPPTDEPLEKGYSHQINVMCEFL 480
Db 421 KVEFSQYNDQTDASTQYDTSKRNGAVSWDSIDQLPPTDEPLEKGYSHQINVMCEFL 480
QY 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQLPLVAKYKQSGASVYAGPRFTGGDIIOC 540
Db 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQLPLVAKYKQSGASVYAGPRFTGGDIIOC 540
QY 541 TENGSAATIVTPDVASQYKRYARIHYASTQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
Db 541 TENGSAATIVTPDVASQYKRYARIHYASTQITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNILASFSTPELSCNNLQIGVTGLSAGDKYIDKIEFIPVN 644
Db 601 YNSFNILASFSTPELSCNNLQIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 4
AAP95585
ID AAP95585 standard; protein; 644 AA.
AC AAP95585;
XX 08-AUG-1990 (first entry)
XX M-7 crystal toxin.
XX M-7 toxin crystal; Coleoptera; beetle.
XX Bacillus thuringiensis strain san-diego (NRRL B-15939).
XX US4853331-A.
XX 01-AUG-1989.
XX 30-NOV-1988; 88US-0278292.
XX 16-AUG-1985; 85US-0767227.
XX 15-JUL-1988; 88US-0219420.

```

XX (MYCO-) MYCOGEN CORP.
 XX Hernstadt C, Wilcox E;
 XX WPI: 1989-277854/38.
 XX N-PSDB: AAN90957.
 XX Cloning of *Bacillus thuringiensis* toxin gene
 XX for expression of protein toxic to beetles of order Coleoptera.
 XX Disclosure; Page 13-14; 10pp; English.
 XX
 XX The gene encoding the toxin can be cloned and used to produce the
 XX M-7 crystal which has activity against eg western spotted cucumber
 XX beetle, and northern, western and southern corn rootworm.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 3406; DB 10; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPLEDLNFKELRMTADNTEALDSS 60
 Db 1 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPLEDLNFKELRMTADNTEALDSS 60
 Oy 61 TTKDVIQKGISVVDLGVGFPGGALVSFTNFLTNPSEDPKRAFMEOVEALMDOK 120
 Db 61 TTKDVIQKGISVVDLGVGFPGGALVSFTNFLTNPSEDPKRAFMEOVEALMDOK 120
 Oy 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQASHFRNS 180
 Db 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQASHFRNS 180
 Oy 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRROLKLOEYT 240
 Db 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRROLKLOEYT 240
 Oy 241 DHCVKWYNGDLKLRGSSSESVWVFNRRREMTLTVLDLALPLVDVRLPREVATELT 300
 Db 241 DHCVKWYNGDLKLRGSSSESVWVFNRRREMTLTVLDLALPLVDVRLPREVATELT 300
 Oy 301 RDVLTDPYGVNMLRGYGTFSNIENYIRKPHLEDYLRHIOFHTROPQGYGNDSEFNYS 360
 Db 301 RDVLTDPYGVNMLRGYGTFSNIENYIRKPHLEDYLRHIOFHTROPQGYGNDSEFNYS 360
 Oy 361 GNYVSTRPSIGSNDIITSPPYGNKSSPEVONLEFNKEKYRAVANTNLAWPSAVYSGVT 420
 Db 361 GNYVSTRPSIGSNDIITSPPYGNKSSPEVONLEFNKEKYRAVANTNLAWPSAVYSGVT 420
 Oy 421 KVEFSQYNDQTEASTQYDYSKRNVGAVSMDSIDQLPPTDEPLEKGYSHQUNYVMEFL 480
 Db 421 KVEFSQYNDQTEASTQYDYSKRNVGAVSMDSIDQLPPTDEPLEKGYSHQUNYVMEFL 480
 Oy 481 MGSRRCTIYVLTWTHRSVDFENMIDSKITPOLPLVAKAYLQSGASVAVGAPRTGGDIIOC 540
 Db 481 MGSRRCTIYVLTWTHRSVDFENMIDSKITPOLPLVAKAYLQSGASVAVGAPRTGGDIIOC 540
 Oy 541 TENGSAATTYVPDYVSQKYRARIHYASTQITFTLSLDGAPFQOYFDDKINKGDTLT 600
 Db 541 TENGSAATTYVPDYVSQKYRARIHYASTQITFTLSLDGAPFQOYFDDKINKGDTLT 600
 Oy 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIYVN 644
 Db 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIYVN 644

XX 28-JAN-1994 (first entry)
 XX Delta endotoxin.
 XX Endotoxin; *Bacillus*; lice; insecticide; sheep.
 XX *Bacillus thuringiensis* PS40D1.
 XX WO9314641-A.
 XX 05-AUG-1993.
 XX 31-DEC-1992; 92MO-US11337.
 XX 29-JAN-1992; 92US-0828788.
 XX (MYCO) MYCOGEN CORP.
 XX Hickie LA, Payne J;
 XX WPI: 1993-258266/32.
 XX N-PSDB: AAO47288.
 XX Controlling biting lice on sheep - comprises administering
 XX *Bacillus thuringiensis* toxins to host
 XX
 XX Disclosure; Page 31-32; 64pp; English.
 XX
 XX Many strains of *Bacillus thuringiensis* (B.t) produce insecticidal
 XX delta endotoxins. A number of these endotoxins have been found to
 XX be toxic to *Damillia* ovis, the biting louse of sheep. The B.T.
 XX isolates which produce these toxins can be grown and the delta
 XX endotoxin which is produced can be recovered by standard procedures.
 XX The genes encoding these endotoxins can also be transferred to a
 XX suitable host via a recombinant vector and the resulting
 XX transformants used in methods to control lice.
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 3406; DB 14; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1.7e-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPLEDLNFKELRMTADNTEALDSS 60
 Db 1 MNPNNRSEHDITKTENNEVPTNHVOYPLAETPNPLEDLNFKELRMTADNTEALDSS 60
 Oy 61 TTKDVIQKGISVVDLGVGFPGGALVSFTNFLTNPSEDPKRAFMEOVEALMDOK 120
 Db 61 TTKDVIQKGISVVDLGVGFPGGALVSFTNFLTNPSEDPKRAFMEOVEALMDOK 120
 Oy 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQASHFRNS 180
 Db 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQASHFRNS 180
 Oy 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRROLKLOEYT 240
 Db 181 MPFSAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYRROLKLOEYT 240
 Oy 241 DHCVKWYNGDLKLRGSSSESVWVFNRRREMTLTVLDLALPLVDVRLPREVATELT 300
 Db 241 DHCVKWYNGDLKLRGSSSESVWVFNRRREMTLTVLDLALPLVDVRLPREVATELT 300
 Oy 301 RDVLTDPYGVNMLRGYGTFSNIENYIRKPHLEDYLRHIOFHTROPQGYGNDSEFNYS 360
 Db 301 RDVLTDPYGVNMLRGYGTFSNIENYIRKPHLEDYLRHIOFHTROPQGYGNDSEFNYS 360
 Oy 361 GNYVSTRPSIGSNDIITSPPYGNKSSPEVONLEFNKEKYRAVANTNLAWPSAVYSGVT 420
 Db 361 GNYVSTRPSIGSNDIITSPPYGNKSSPEVONLEFNKEKYRAVANTNLAWPSAVYSGVT 420
 Oy 421 KVEFSQYNDQTEASTQYDYSKRNVGAVSMDSIDQLPPTDEPLEKGYSHQUNYVMEFL 480

```

Db 421 KVEFSQYNDQDEASTQYVDSKRNKAVGAVSWDSIDQLPETTDEPLEKGYSHQLNVMCF 480
Oy 481 MGSNGTTPVLWTWTKSVDFEPMIDSKKITQPLVKAVALGASVAVGPRFTGGDIQC 540
Db 481 MGSNGTTPVLWTWTKSVDFEPMIDSKKITQPLVKAVALGASVAVGPRFTGGDIQC 540
Oy 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLLSDGAPFNQYVFDKTIKGDITL 600
Db 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLLSDGAPFNQYVFDKTIKGDITL 600
Oy 601 YNSFNLFASFSTPELFGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLFASFSTPELFGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644

RESULT 6
AAR56697
ID AAR56697 standard; Protein; 644 AA.
AC AAR56697;
XX
DT 27-MAR-1995 (first entry)
XX
DE CryIIIA insecticidal crystal protein.
XX
KW CryIIA; CryIIIB; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;
KW lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
XX probe; hybridisation.
XX
OS Bacillus thuringiensis.
XX
PN US5338544-A.
XX
PD 16-AUG-1994.
XX
PF 16-APR-1987; 87US-0039542.
XX
PR 16-APR-1987; 87US-0039542.
PR 11-JUL-1989; 89US-0379015.
PR 28-AUG-1991; 91US-0751452.
PR 26-FEB-1993; 93US-0023736.

XX (ECOG-) ECOGEN INC.
XX
PA Donovan WP;
XX
PI
XX
DR WPI; 1994-263236/32.
DR N-PDB; AAQ71026.
XX
PT New Cry IIB protein - obcd, from the cry II B gene in Bacillus
PT thuringiensis var. Kurstaki, active against lepidopteran insects
XX
PS Example 7; Fig 4A-4D; 39pp; English.
XX
XX This sequence shows the amino acid sequence of CryIIIA protein. The
XX promoter from the CryIIIA gene sequence was fused to the protein
XX coding region of the CryIIB gene (AAQ71027). The recombinant hybrid
XX fusion gene expressed the CryIIB crystal protein more efficiently
XX than its native promoter. CryIIB encodes an insecticidal crystal
XX protein isolated from Bacillus thuringiensis var. kurstaki. It
XX produces crystal proteins during sporulation which are specifically
XX toxic to certain orders and species of insects, esp. lepidoptera.
XX CryIIB can be used in compositions used as environmentally acceptable
XX insecticides. (See also AAR56696 and AAR56698)
XX
SQ Sequence 644 AA;
Query Match 100.0%; Score 3406; DB 15; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.7e-268;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MNPNNRSEHDITKTENNEVPTNHOVPLAETPPTLEDLNVKREFLMNTADNTEALDSS 60

```

```

Db 1 MNPNNRSEHDITKTENNEVPTNHOVPLAETPPTLEDLNVKREFLMNTADNTEALDSS 60
Oy 61 TTKVIOKIGISVVDLDLVGFPEFGALVSEYTFELNTIMPSEDPMKAFMEQVEALNDQK 120
Db 61 TTKVIOKIGISVVDLDLVGFPEFGALVSEYTFELNTIMPSEDPMKAFMEQVEALNDQK 120
Oy 121 IADYAKNKALAELOGLONNVEDVYSAISSWQKNFVSSRNPHSGRIEELSQAESHRRNS 180
Db 121 IADYAKNKALAELOGLONNVEDVYSAISSWQKNFVSSRNPHSGRIEELSQAESHRRNS 180
Oy 181 MPFALISGEYVLFITTYQAANTHLFLKDAQITGEEGKEKEDIAEFTYKQNLQDEYT 240
Db 181 MPFALISGEYVLFITTYQAANTHLFLKDAQITGEEGKEKEDIAEFTYKQNLQDEYT 240
Oy 241 DHCVMKYNVGLDKLGSSESVNENRNRREMTLVLDLAFPLYDVRLYPKREKTELT 300
Db 241 DHCVMKYNVGLDKLGSSESVNENRNRREMTLVLDLAFPLYDVRLYPKREKTELT 300
Oy 301 RDVLTDPVIGVNNLRGCTTSNENYTRKPHLEDYLHRIOPHTRFQGYGNDSPYWS 360
Db 301 RDVLTDPVIGVNNLRGCTTSNENYTRKPHLEDYLHRIOPHTRFQGYGNDSPYWS 360
Oy 361 GMYSTRPSIGSNDITTSPEYGNKSESPVONLEFNGEKYRAVANTNLAVPSAVYSGYT 420
Db 361 GMYSTRPSIGSNDITTSPEYGNKSESPVONLEFNGEKYRAVANTNLAVPSAVYSGYT 420
Oy 421 KVEFSQYNDQDEASTQYVDSKRNKAVGAVSWDSIDQLPETTDEPLEKGYSHQLNVMCF 480
Db 421 KVEFSQYNDQDEASTQYVDSKRNKAVGAVSWDSIDQLPETTDEPLEKGYSHQLNVMCF 480
Oy 481 MGSNGTTPVLWTWTKSVDFEPMIDSKKITQPLVKAVALGASVAVGPRFTGGDIQC 540
Db 481 MGSNGTTPVLWTWTKSVDFEPMIDSKKITQPLVKAVALGASVAVGPRFTGGDIQC 540
Oy 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLLSDGAPFNQYVFDKTIKGDITL 600
Db 541 TENGSAATITVYPDVYSQKRYARIRHYASTSQITFTLLSDGAPFNQYVFDKTIKGDITL 600
Oy 601 YNSFNLFASFSTPELFGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLFASFSTPELFGNNLQIGVTGLSAGDKVYIDKIEFTIPVN 644

RESULT 7
AAR56698
ID AAR56698 standard; Protein; 644 AA.
AC AAR56698;
XX
DT 27-MAR-1995 (first entry)
XX
DE CryIIB insecticidal crystal protein.
XX
KW CryIIA; CryIIIB; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;
KW lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
XX probe; hybridisation.
XX
OS Bacillus thuringiensis.
XX
PN US5338544-A.
XX
PD 16-AUG-1994.
XX
PF 16-APR-1987; 87US-0039542.
XX
PR 16-APR-1987; 87US-0039542.
PR 11-JUL-1989; 89US-0379015.
PR 28-AUG-1991; 91US-0751452.
PR 26-FEB-1993; 93US-0023736.

XX (ECOG-) ECOGEN INC.
XX

```

PI Donovan WP;
 XX WPI: 1994-263236/32.
 DR N-PSDB; AA071027.
 XX
 PT New Cry IIB protein - obtd. from the cry II B gene in *Bacillus*
 PT thuringiensis var. *Kurstaki*, active against lepidopteran insects
 XX
 XX Claim 1; Flg 6A-6D; 39pp; English.
 XX
 CC This sequence shows the amino acid sequence of CryIIB protein. The
 CC promoter from the CryIIA gene (AA071026) sequence was fused to the
 CC protein coding region of the CryIIB gene. The recombinant hybrid
 CC fusion gene expressed the CryIIB crystal protein more efficiently
 CC than its native promoter. CryIIB encodes an insecticidal crystal
 CC protein isolated from *Bacillus thuringiensis* var. *Kurstaki*. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. Lepidopterans.
 CC CryIIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR56696 and AAR56698)
 CC
 XX
 SQ Sequence 644 AA;

Query Match 100.0%; Score 3406; DB 15; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1,76-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNNEPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNNEPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 QY 61 TTKDVIQKGISVVGDLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVGDLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 120
 QY 121 IDYAKNKKALAELOGKNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 DB 121 IDYAKNKKALAELOGKNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 QY 181 MSPAISGCEVLETTYQAQANTHLEFLKDAQIYGEWGEYKEKEDAEFYKROKLTQOXYT 240
 DB 181 MSPAISGCEVLETTYQAQANTHLEFLKDAQIYGEWGEYKEKEDAEFYKROKLTQOXYT 240
 QY 241 DHCQWYNNGLDKLGSSSESVNNRRIRREKTLTVLDLALFPLYDVRLYKPEVTELT 300
 DB 241 DHCQWYNNGLDKLGSSSESVNNRRIRREKTLTVLDLALFPLYDVRLYKPEVTELT 300
 QY 301 RDVLTPITGVNLLRGYGTETSENIENYIRKPLFDYLRHIOFHRPFGYGNDSFNWWS 360
 DB 301 RDVLTPITGVNLLRGYGTETSENIENYIRKPLFDYLRHIOFHRPFGYGNDSFNWWS 360
 QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLFEFNGEKYRAVANTNLAVPSAVSGVT 420
 DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLFEFNGEKYRAVANTNLAVPSAVSGVT 420
 QY 421 KYEFQYNDQDEASTQYITDSKRNGAVSMISIDLPETDEPLEKGYSHQLWYVWCF 480
 DB 421 KYEFQYNDQDEASTQYITDSKRNGAVSMISIDLPETDEPLEKGYSHQLWYVWCF 480
 QY 481 MOGSHGTTPLVLTWTHKSVDFNMIDSKKITQPLVKAATKQSGASVAVAGPFTGDIIOC 540
 DB 481 MOGSHGTTPLVLTWTHKSVDFNMIDSKKITQPLVKAATKQSGASVAVAGPFTGDIIOC 540
 QY 541 TENGAATITVTPDVYSQKTRAKRHVASTISQITFTSLDGAFFNOYFFDKTINKGDTLT 600
 DB 541 TENGAATITVTPDVYSQKTRAKRHVASTISQITFTSLDGAFFNOYFFDKTINKGDTLT 600
 QY 601 YNSFNILASFSTPELGSNNLQIGVTLGAGDKYVITDIIEFIPVN 644
 DB 601 YNSFNILASFSTPELGSNNLQIGVTLGAGDKYVITDIIEFIPVN 644

RESULT 8

AAV23214
 ID AAV23214 standard; Protein; 652 AA.
 XX
 AC AAV23214;
 XX
 DT 24-AUG-1999 (first entry)
 XX
 DE Amino acid sequence of Cry3A protein.
 XX
 KW Cry3Bb; mutant; insecticidal activity; insecticidal specificity;
 KW coleoptera; southern corn rootworm; western corn root worm; Cry3A;
 KW Diabrotica undecimpunctata howardi Barber; transgenic plant;
 KW Diabrotica virgifera virgifera Leconte; insecticide resistance.
 OS
 XX *Bacillus thuringiensis*.
 XX
 PM W09331248-A1.
 PD 24-JUN-1999.
 XX
 PE 17-DEC-1998; 98WO-0526852.
 XX
 PR 18-DEC-1997; 97US-0996441.
 PR 18-DEC-1997; 97US-0993170.
 PR 18-DEC-1997; 97US-0993722.
 PR 18-DEC-1997; 97US-0993775.
 XX
 PA (ECOG-) ECOGEN INC.
 PA (MONS) MONSANTO CO.
 XX
 PI Brusseck SM, Bryson JW, English L, Kulesza CA, Malvar TM;
 PI Romano C, Slatin SL, Von Tersch MA, Walters FS;
 XX
 DR WPI: 1999-395184/33.
 XX
 XX Insecticidal *Bacillus thuringiensis* proteins
 PT
 PS Disclosure; Page 505-507; 512pp; English.
 XX
 CC The present sequence represents the Cry3A protein. The specification
 CC describes new *Bacillus thuringiensis* Cry3Bb mutant proteins, and
 CC provides methods for producing them. The B. *thuringiensis* Cry3Bb
 CC polypeptide was modified to have improved insecticidal activity or
 CC enhanced insecticidal specificity against a target insect. The
 CC modification comprises at least one amino acid substitution, addition,
 CC or deletion in the primary sequence of the native or unmodified Cry3Bb
 CC polypeptide, wherein the substitution or deletion occurs at a position
 CC corresponding to from about amino acids 1-365 of the unmodified
 CC polypeptide sequence (AAV23207 represents the wild type Cry3Bb
 CC protein). The polypeptide can be used to kill coleopteran pests,
 CC especially by application to the environment. It is especially
 CC useful against southern corn rootworm and western corn root worm,
 CC (*Diabrotica undecimpunctata* howardi Barber, and *Diabrotica virgifera*
 CC *virgifera* Leconte respectively). The mutant cry3Bb polynucleotides
 CC can also be used to produce transgenic plants with increased
 CC insecticide resistance.
 CC
 XX
 SQ Sequence 652 AA;

Query Match 100.0%; Score 3406; DB 20; Length 652;
 Best Local Similarity 100.0%; Pred. No. 1,76-268;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNNEPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 9 MNPNNRSEHDITKTENNNEPTNHVOYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 68
 QY 61 TTKDVIQKGISVVGDLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 120
 DB 69 TTKDVIQKGISVVGDLGVVGFPGGALVSFTNPLNTIMPSEDPMKAFMEQVEALMDOK 128
 QY 121 IDYAKNKKALAELOGKNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180
 DB 121 IDYAKNKKALAELOGKNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLFSQASHFRNS 180

DB 129 IADYAKNKALAELOGLONNVEDYVSALSSWOKNPVSSRNPHSGRIRELFSQASHFRNS 188
 QY 181 MPEFAISGEYVLEFITYAQAANTHFLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
 DB 189 MPEFAISGEYVLEFITYAQAANTHFLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 248
 QY 241 DHCVMKYNVGLDKLGGSSYESVWNNRRYRREMTLVLDLALFPLYDRLPKYKTELT 300
 DB 249 DHCVMKYNVGLDKLGGSSYESVWNNRRYRREMTLVLDLALFPLYDRLPKYKTELT 308
 QY 301 RDVLDPDPIGVANNLNGYGTTFSENIENTYRKPHLPDYLRHIOFHRPOFGYNDSPFNWS 360
 DB 309 RDVLDPDPIGVANNLNGYGTTFSENIENTYRKPHLPDYLRHIOFHRPOFGYNDSPFNWS 368
 QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANTNLAVPSAVYSGVT 420
 DB 369 GNYVSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANTNLAVPSAVYSGVT 428
 QY 421 KYEFSQYNDQDEASTQYIDSKRNNGAVSWDSIDOLPETTDEPLEKYSHQALTYMCF 480
 DB 429 KYEFSQYNDQDEASTQYIDSKRNNGAVSWDSIDOLPETTDEPLEKYSHQALTYMCF 488
 QY 481 MGSRGITPVLWTHTKSVDFEWMIDSKITOLPLVKAAYKLOGASVAVAGPRTGGDIIOC 540
 DB 489 MGSRGITPVLWTHTKSVDFEWMIDSKITOLPLVKAAYKLOGASVAVAGPRTGGDIIOC 548
 QY 541 TENGSAATITVTPDVYSOKYRARIHYASTQITFTLSLDGAPNOYFEDKTIKNGDTLT 600
 DB 549 TENGSAATITVTPDVYSOKYRARIHYASTQITFTLSLDGAPNOYFEDKTIKNGDTLT 608
 QY 601 YNSFNLAISTPELISGNNLQIGYGLSAGDKVYIDKIEFIYVN 644
 DB 609 YNSFNLAISTPELISGNNLQIGYGLSAGDKVYIDKIEFIYVN 652

RESULT 9
 AAR99960
 ID AAR99960 standard; Protein: 644 AA.
 AC AAR99960;
 XX
 DT 04-DEC-1996 (first entry)
 XX
 DE B.t.t. coleopteran toxin (alternative N- and C-terminal truncations).
 XX
 KW Bacillus thuringiensis var. tenebrionis; insect resistance;
 KW transgenic plant; crop protection; crystal protein; toxin;
 KW Coleoptera.
 XX
 OS Bacillus thuringiensis var. tenebrionis.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 48
 FT MISC-difference /note= "N-terminus of construct 5456"
 FT MISC-difference 77
 FT MISC-difference /note= "N-terminus of construct 5452"
 FT MISC-difference 99
 FT MISC-difference /note= "N-terminus of construct 5467"
 FT MISC-difference 490
 FT MISC-difference /note= "C-terminus of construct 5438"
 FT MISC-difference 536
 FT MISC-difference /note= "C-terminus of construct 5441"
 FT MISC-difference 582
 FT MISC-difference /note= "C-terminus of construct 5449"
 FT MISC-difference 640
 FT MISC-difference /note= "C-terminus of construct 5448"
 XX
 PN EP731170-A1.
 XX
 PD 11-SEP-1996.
 XX
 PF 26-APR-1988: 8SEP-0870070.

PR 29-APR-1987: 87US-0044081.
 XX (MONS) MONSANTO CO.
 XX
 XX
 PI Fischhoff DA, Fuchs RL, Lavrik PB, McPherson SA;
 PI Perlak FJ;
 XX WPI: 1996-403991/41.
 DR
 XX
 XX
 PT Chimeric plant gene which expresses a Bacillus thuringiensis toxin
 PT protein - useful for prodn. of plants which are toxic to
 PT Coleopteran insects
 XX
 XX
 XX Disclosure: Fig 10; 72pp; English.
 XX
 XX
 CC The effects of N- and C-terminal deletions (AAR99960) on the toxicity
 CC of the Coleopteran toxin (see also AAR99958) of Bacillus thuringiensis
 CC var. tenebrionis (B.t.t.) were examined. Mutant genes were expressed
 CC in E. coli and the truncated proteins were tested for activity against
 CC Colorado potato beetle. All the C-terminal truncations, even of
 CC only 4 amino acids (construct 5448), resulted in a loss of activity.
 CC The N-terminus of the toxin was more tolerant; a mutant toxin
 CC deleted of 76 amino acids (construct 5452) exhibited toxicity.
 CC However, a deletion of 99 amino acids (construct 5467) resulted in
 CC loss of activity.
 CC
 XX
 S0 Sequence 644 AA;
 Query Match 99.9%; Score 3403; DB 17; Length 644;
 Best Local Similarity 99.8%; Pred. No. 2.9e-268;
 Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPNRSEHDITKTENNEVPTNHVQPLAETPPTLEDLNYKEFLMTADNTEALDSS 60
 DB 1 MNPNRSEHDITKTENNEVPTNHVQPLAETPPTLEDLNYKEFLMTADNTEALDSS 60
 QY 61 TTKDYIOKGISVGDILGVGPPGGALVSYTYNPLNTWPSSEPMKAFMQVYALMDOK 120
 DB 61 TTKDYIOKGISVGDILGVGPPGGALVSYTYNPLNTWPSSEPMKAFMQVYALMDOK 120
 QY 121 IADYAKNKALAELOGLONNVEDYVSALSSWOKNPVSSRNPHSGRIRELFSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWOKNPVSSRNPHSGRIRELFSQASHFRNS 180
 QY 181 MPEFAISGEYVLEFITYAQAANTHFLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
 DB 181 MPEFAISGEYVLEFITYAQAANTHFLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
 QY 241 DHCVMKYNVGLDKLGGSSYESVWNNRRYRREMTLVLDLALFPLYDRLPKYKTELT 300
 DB 241 DHCVMKYNVGLDKLGGSSYESVWNNRRYRREMTLVLDLALFPLYDRLPKYKTELT 300
 QY 301 RDVLDPDPIGVANNLNGYGTTFSENIENTYRKPHLPDYLRHIOFHRPOFGYNDSPFNWS 360
 DB 301 RDVLDPDPIGVANNLNGYGTTFSENIENTYRKPHLPDYLRHIOFHRPOFGYNDSPFNWS 360
 QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANTNLAVPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSPEVONLEFNGEKYRAVANTNLAVPSAVYSGVT 420
 QY 421 KYEFSQYNDQDEASTQYIDSKRNNGAVSWDSIDOLPETTDEPLEKYSHQALTYMCF 480
 DB 421 KYEFSQYNDQDEASTQYIDSKRNNGAVSWDSIDOLPETTDEPLEKYSHQALTYMCF 480
 QY 481 MGSRGITPVLWTHTKSVDFEWMIDSKITOLPLVKAAYKLOGASVAVAGPRTGGDIIOC 540
 DB 481 MGSRGITPVLWTHTKSVDFEWMIDSKITOLPLVKAAYKLOGASVAVAGPRTGGDIIOC 540
 QY 541 TENGSAATITVTPDVYSOKYRARIHYASTQITFTLSLDGAPNOYFEDKTIKNGDTLT 600
 DB 541 TENGSAATITVTPDVYSOKYRARIHYASTQITFTLSLDGAPNOYFEDKTIKNGDTLT 600
 QY 601 YNSFNLAISTPELISGNNLQIGYGLSAGDKVYIDKIEFIYVN 644

```

|||||
Db      601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPVN 644
RESULT 10
AAW34817
ID      AAW34817 standard; Protein: 644 AA.
AC      AAW34817;
XX      25-FEB-1998 (first entry)
DE      Novel CryIIIA mutant protein SA13A.
XX      CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW      increased toxicity; Coleopteran insect; Colorado potato beetle;
KM      relative solvent accessibility; plant resistance;
XX      Diabrotica virgifera virgifera.
OS      Synthetic.
XX      Bacillus thuringiensis.
FH      Key
FT      Location/Qualifiers
FT      MISC-difference 413
FT      /label= S413A
FT      /note= "wild type Ser replaced with Ala"
XX      US5659123-A.
XX      19-AUG-1997.
XX      26-AUG-1994: 94US-0295060.
XX      26-AUG-1994: 94US-0295060.
XX      26-AUG-1994: 94US-0295060.
XX      (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX      Jansens S, Peferoen M, Van Rie J;
XX      WPI; 1997-424316/39.
XX      Modified Bacillus thuringiensis CryIII proteins - with increased
PT      toxicity against insect pests, particularly Coleopteran insects,
PT      e.g. corn rootworm and Colorado potato beetle
XX      Example 1; Page : 22pp; English.
XX      Novel CryIIIA proteins AAW3481-41 were produced by alanine scanning
CC      mutagenesis of domain II of the CryIIIA protein of Bacillus
CC      thuringiensis. All the positions changed to alanine in these proteins
CC      are located in some of the solvent exposed loops and beta-strands
CC      directed towards or located at the molecular apex. The substituted amino
CC      acids have a relative solvent accessibility of at least 40%, or are a
CC      maximum distance of 3 amino acids away from an amino acid having at least
CC      40% relative solvent accessibility. The novel CryIIIA proteins have an
CC      increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC      and can be used to combat, or improve plant resistance towards insects.
CC      Specifically, the toxicity of the present sequence towards Diabrotica
CC      virgifera virgifera was tested. The EC50 value (concentration at which
CC      50% feeding inhibition is observed) of the present protein was found to
CC      be 1.93 microgram per millilitre, compared to 5.55 microgram per
CC      millilitre for the wild type CryIIIA protein.
CC      note: this sequence does not appear in the specification; it was created
CC      using information provided.
XX      Sequence 644 AA.
SO
Query Match 99.9%; Score 3403; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 2,9e-268;
Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 MNPNNRSEHDTIKTENNEVPTNNHVOYPLAETPNPTLEDNLNKEFLRMTADNNTALDSS 60
|||||

```

```

Db      1 MNPNNRSEHDTIKTENNEVPTNNHVOYPLAETPNPTLEDNLNKEFLRMTADNNTALDSS 60
QY      61 TTKDVIQKIGISVGDLLGVGPFEGGALVSFTNPLNTIMPSEDPWKAFMEOVALMDOK 120
Db      61 TTKDVIQKIGISVGDLLGVGPFEGGALVSFTNPLNTIMPSEDPWKAFMEOVALMDOK 120
QY      121 IADYAKNRKALAELOGLQNNVEDYVSALSSWQKNPVSSNRNPHSOGRIREFSQASHFRNS 180
Db      121 IADYAKNRKALAELOGLQNNVEDYVSALSSWQKNPVSSNRNPHSOGRIREFSQASHFRNS 180
QY      181 MPEFALISGEVLEFLTYAQAANTHFLFKDAQIYGEEMGKEDIAEFYKQKLLTOEYT 240
Db      181 MPEFALISGEVLEFLTYAQAANTHFLFKDAQIYGEEMGKEDIAEFYKQKLLTOEYT 240
QY      241 DHCVMWVNGDLDKLGSSYESWVNNRFRREMTLVLDLILFPLYDVRILPKKVEKLELT 300
Db      241 DHCVMWVNGDLDKLGSSYESWVNNRFRREMTLVLDLILFPLYDVRILPKKVEKLELT 300
QY      301 RDVLTDPIVGVNNLNGYGTFSNIENYIRKPHLEFDYLRHQFHTRFQGYGNDSPNWS 360
Db      301 RDVLTDPIVGVNNLNGYGTFSNIENYIRKPHLEFDYLRHQFHTRFQGYGNDSPNWS 360
QY      361 GNYVSTRPSIGSNDIITSPFGNKSSEPVQNLERNGEKVVYAAVANTNLAVPSSVSGVT 420
Db      361 GNYVSTRPSIGSNDIITSPFGNKSSEPVQNLERNGEKVVYAAVANTNLAVPSSVSGVT 420
QY      421 KVEFSQYNDQDDEASTQYDYSKRNGAVSWDSIDQLPETTDEPLEKYSHQLVYVNCFL 480
Db      421 KVEFSQYNDQDDEASTQYDYSKRNGAVSWDSIDQLPETTDEPLEKYSHQLVYVNCFL 480
QY      481 MGSRGITPVLTWTHKSVDFENMIDSKKITQLPLVKAVKILOGSAYVAGPFTGDIIOC 540
Db      481 MGSRGITPVLTWTHKSVDFENMIDSKKITQLPLVKAVKILOGSAYVAGPFTGDIIOC 540
QY      541 TENGSAATITVTPDYSOKYRARIHVASTQITFTSLDAPRNQYFFDKTINKGTLT 600
Db      541 TENGSAATITVTPDYSOKYRARIHVASTQITFTSLDAPRNQYFFDKTINKGTLT 600
QY      601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPVN 644
Db      601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIPVN 644
RESULT 11
AAW34827
ID      AAW34827 standard; Protein: 644 AA.
XX      AAW34827;
XX      25-FEB-1998 (first entry)
DE      Novel CryIIIA mutant protein S385A.
XX      CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW      increased toxicity; Coleopteran insect; Colorado potato beetle;
KM      relative solvent accessibility; plant resistance;
XX      Diabrotica virgifera virgifera.
OS      Synthetic.
XX      Bacillus thuringiensis.
FH      Key
FT      Location/Qualifiers
FT      MISC-difference 385
FT      /label= S385A
FT      /note= "wild type Ser replaced with Ala"
XX      US5659123-A.
XX      19-AUG-1997.
XX      26-AUG-1994: 94US-0295060.
XX      26-AUG-1994: 94US-0295060.
XX      26-AUG-1994: 94US-0295060.
PR

```

XX (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 XX WPI: 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1; Page -; 22p; English.
 XX
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 0.78 microgram per millilitre, compared to 2.88 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 SQ Sequence 644 AA:
 Query Match 99.9%; Score 3403; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 2.9e-268;
 Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPNNRSEHDTIKTTENNEVPINHOYPLAETPNPLEDLNFKELMTADNTEALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPINHOYPLAETPNPLEDLNFKELMTADNTEALDSS 60
 QY 61 TTKDVIOKGISVVDLLGVGFPFGCALVSFTYNFLNTIPSDPKAFMEYVLEALMDOK 120
 DB 61 TTKDVIOKGISVVDLLGVGFPFGCALVSFTYNFLNTIPSDPKAFMEYVLEALMDOK 120
 QY 121 IADYAKKALAELOGLONNEDVYSAISSMOKNPVSSRNHSGRIRELSQAESHRNS 180
 DB 121 IADYAKKALAELOGLONNEDVYSAISSMOKNPVSSRNHSGRIRELSQAESHRNS 180
 QY 181 MPSEFAISGEVLELTYYAQAANTHLLFLKDAQIYGEEMGEKEDIAEFYKROKLQDEYT 240
 DB 181 MPSEFAISGEVLELTYYAQAANTHLLFLKDAQIYGEEMGEKEDIAEFYKROKLQDEYT 240
 QY 241 DHCYKRWNVGLDKRGSSYSESWVFNRYRREMTTVLDLALPPLYVRLXPYEVKTEL 300
 DB 241 DHCYKRWNVGLDKRGSSYSESWVFNRYRREMTTVLDLALPPLYVRLXPYEVKTEL 300
 QY 301 RDVLTDPVIGVNNLRGCTFESNIENYIRKPHLFYLRHQFHTRFQPGYVGNDSFYWMS 360
 DB 301 RDVLTDPVIGVNNLRGCTFESNIENYIRKPHLFYLRHQFHTRFQPGYVGNDSFYWMS 360
 QY 361 GNVYSTRPSTISNDITSPFYGNKSSEPVONLEPNGEKTRAVANNTLAWPSPAVISGVY 420
 DB 361 GNVYSTRPSTISNDITSPFYGNKSSEPVONLEPNGEKTRAVANNTLAWPSPAVISGVY 420
 QY 421 KVESSQVNDQDEASTQYOSKRNVGAVSMDSIDLPEPTDEPLEKGYSHQLVWVCF 480
 DB 421 KVESSQVNDQDEASTQYOSKRNVGAVSMDSIDLPEPTDEPLEKGYSHQLVWVCF 480
 QY 481 MQGSRGTIPVLTWTHKSVDFNMDSKKITQPLVKAAYKLQSGASVYAGPFTGGDIIQC 540
 DB 481 MQGSRGTIPVLTWTHKSVDFNMDSKKITQPLVKAAYKLQSGASVYAGPFTGGDIIQC 540

QY 541 TENGSAATIIYTPDVYSQKTRARIHASTSQTITFTLSLDCAPPNOYFPDKTINKGDTLT 600
 DB 541 TENGSAATIIYTPDVYSQKTRARIHASTSQTITFTLSLDCAPPNOYFPDKTINKGDTLT 600
 QY 601 YNSFNLASFSPTPELSGNNLQIGVTLGASGKVKYIDKTEFIPVN 644
 DB 601 YNSFNLASFSPTPELSGNNLQIGVTLGASGKVKYIDKTEFIPVN 644
 RESULT 12
 AAW34829
 ID AAW34829 standard; Protein: 644 AA.
 XX
 AC AAW34829;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein S449A.
 XX
 KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH Key Location/Qualifiers
 FT Misc-difference 449
 FT //label= "S449A
 FT /note= "wild type Ser replaced with Ala"
 FT
 FT
 FT
 PN US5659123-A.
 XX
 PD 19-AUG-1997.
 XX
 PE 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 XX WPI: 1997-424316/39.
 DR
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1; Page -; 22p; English.
 XX
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 7.12 microgram per millilitre, compared to 4.04 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 SQ Sequence 644 AA:
 Query Match 99.9%; Score 3403; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 2.9e-268;
Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDLNYKFEFLMTADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDLNYKFEFLMTADNNTALDSS 60
QY 61 TTKDYIOKGISVGDLLGVGPPGALVSFYTNFLMTWPSDEDPWKAPEQVEALMDOK 120
DB 61 TTKDYIOKGISVGDLLGVGPPGALVSFYTNFLMTWPSDEDPWKAPEQVEALMDOK 120
QY 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIRLELSQAESHFRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIRLELSQAESHFRNS 180
QY 181 MPSPAIISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQKLQOERYT 240
DB 181 MPSPAIISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQKLQOERYT 240
QY 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPLDYRLYPREVTELT 300
DB 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPLDYRLYPREVTELT 300
QY 301 RDVLTDPVGVNNLRGCGTFESNIENYIRKPHLEDFYLRHQFHTRQPGYGGNDSFNYS 360
DB 301 RDVLTDPVGVNNLRGCGTFESNIENYIRKPHLEDFYLRHQFHTRQPGYGGNDSFNYS 360
QY 361 GNYVSTRPSIGSNDIITSPYGNKSSPVONLEFNCKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDIITSPYGNKSSPVONLEFNCKYRAVANNTLAWPSAVYSGVT 420
QY 421 KVERSOYNDQTDASTQYDSKRNKVGAVSWDSIDQLPPTTDBPLEKGYSHQNTYMCFL 480
DB 421 KVERSOYNDQTDASTQYDSKRNKVGAVSWDSIDQLPPTTDBPLEKGYSHQNTYMCFL 480
QY 481 MGSRGITPVLWTNHSVDFNMDISKITQPLVKAAYKQSGASVYAGPRFTGGDIIOC 540
DB 481 MGSRGITPVLWTNHSVDFNMDISKITQPLVKAAYKQSGASVYAGPRFTGGDIIOC 540
QY 541 TENGSAAITVTPDVYSQKRYRARIHYASTSQITFTLSLDGAPNOYFEDKTIKNGDTLT 600
DB 541 TENGSAAITVTPDVYSQKRYRARIHYASTSQITFTLSLDGAPNOYFEDKTIKNGDTLT 600
QY 601 YNSFNLFASFTEPPELSGNNLOIGVTGLSAGDKYIDKIEFIPVN 644
DB 601 YNSFNLFASFTEPPELSGNNLOIGVTGLSAGDKYIDKIEFIPVN 644

RESULT 13
AAM34841
ID AAM34841 standard; Protein; 644 AA.
XX
AC AAM34841;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein S442A.
XX
KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW diabrotica virgifer a virgifer a; plant resistance;
XX
OS Synthetic.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 442 /Label= S442A
FT /note= "wild type Ser replaced with Ala"
XX
XX US5659123-A.

```

```

PD 19-AUG-1997.
XX
PF 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLB2) PLANT GENETIC SYSTEMS NV.
XX
PI Jansens S, Peferoen M, Van Rie J;
XX
XX WPI; 1997-424316/39.
XX
DR Modified Bacillus thuringiensis CryIIA proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
PS Claim 9; Page -: 22pp; English.
XX
CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifer a was tested, and the present mutant protein was
CC found to be a "down mutant" for Diabrotica virgifer a. The
CC toxicity of the mutant protein for this Diabrotica pest was
CC significantly below the toxicity of the native CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA:

Query Match 99.9%; Score 3403; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 2.9e-268;
Matches 643; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDLNYKFEFLMTADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDLNYKFEFLMTADNNTALDSS 60
QY 61 TTKDYIOKGISVGDLLGVGPPGALVSFYTNFLMTWPSDEDPWKAPEQVEALMDOK 120
DB 61 TTKDYIOKGISVGDLLGVGPPGALVSFYTNFLMTWPSDEDPWKAPEQVEALMDOK 120
QY 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIRLELSQAESHFRNS 180
DB 121 IADYAKNKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIRLELSQAESHFRNS 180
QY 181 MPSPAIISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQKLQOERYT 240
DB 181 MPSPAIISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQKLQOERYT 240
QY 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPLDYRLYPREVTELT 300
DB 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPLDYRLYPREVTELT 300
QY 301 RDVLTDPVGVNNLRGCGTFESNIENYIRKPHLEDFYLRHQFHTRQPGYGGNDSFNYS 360
DB 301 RDVLTDPVGVNNLRGCGTFESNIENYIRKPHLEDFYLRHQFHTRQPGYGGNDSFNYS 360
QY 361 GNYVSTRPSIGSNDIITSPYGNKSSPVONLEFNCKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDIITSPYGNKSSPVONLEFNCKYRAVANNTLAWPSAVYSGVT 420
QY 421 KVERSOYNDQTDASTQYDSKRNKVGAVSWDSIDQLPPTTDBPLEKGYSHQNTYMCFL 480
DB 421 KVERSOYNDQTDASTQYDSKRNKVGAVSWDSIDQLPPTTDBPLEKGYSHQNTYMCFL 480

```


QY 481 MGSRGITPVLTHKSVDFNMIDSKITQLPVKAYKLGASVAGPFTGGDIQC 540
 DB 481 MGSRGITPVLTHKSVDFNMIDSKITQLPVKAYKLGASVAGPFTGGDIQC 540
 QY 541 TENGSAATITVTPDVYSQKRYARIRHYASTSQITFTLSLDGAPFNOYFEDKTIKNGDILT 600
 DB 541 TENGSAATITVTPDVYSQKRYARIRHYASTSQITFTLSLDGAPFNOYFEDKTIKNGDILT 600
 QY 601 YNSFNLASFSTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 14
 AAW34822
 ID AAW34822 standard; Protein: 644 AA.
 AC AAW34822;
 XX 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein V311A.
 XX
 KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 311 /label- V311A
 FT /note- "wild type Val replaced with Ala"
 XX
 PN US5659123-A.
 PD 19-AUG-1997.
 XX
 PF 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 XX WPI: 1997-424316/39.
 DR
 XX Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 PS
 PS Example 1; Page -; 22pp; English.
 XX
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.09 microgram per millilitre, compared to 1.21 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created

CC using information provided.
 XX
 SQ Sequence 644 AA;
 Query Match 99.9%; Score 3402; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 3.5e-268;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENPTNHNVOYPLAETPPTEDLNKFEELMTADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNENPTNHNVOYPLAETPPTEDLNKFEELMTADNNTALDSS 60
 QY 61 TTKDVYQKGISVVDGLGCVFPFGGALVSFTYFPLNTIMPSEDPKAFNBOYBALMDOK 120
 DB 61 TTKDVYQKGISVVDGLGCVFPFGGALVSFTYFPLNTIMPSEDPKAFNBOYBALMDOK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNVSNNPSQGRIRIELSOAESHRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNVSNNPSQGRIRIELSOAESHRNS 180
 QY 181 MPFAISGVEVLFITTYAQAANTHLFLKDAQIYGEENGKEKEDIAEYKROKLTQOET 240
 DB 181 MPFAISGVEVLFITTYAQAANTHLFLKDAQIYGEENGKEKEDIAEYKROKLTQOET 240
 QY 241 DHCYKMWVGLDKLRGSSYESWVNFNRYRBMTLTVLDLALFPLVYRLYPKKVEKTELT 300
 DB 241 DHCYKMWVGLDKLRGSSYESWVNFNRYRBMTLTVLDLALFPLVYRLYPKKVEKTELT 300
 QY 301 RDVLTPDIYGVNNLRGVTFSTNENTYRKRPHLDYLRHIOFHTRPQGYGNDSPYWS 360
 DB 301 RDVLTPDIYGVNNLRGVTFSTNENTYRKRPHLDYLRHIOFHTRPQGYGNDSPYWS 360
 QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLFEENGKEKRYRAVANTNLAVPSAVSGVT 420
 DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLFEENGKEKRYRAVANTNLAVPSAVSGVT 420
 QY 421 KYVESQYNDQDDEASTQTYDSKRNVAWSIDQLPETTDEPLEKGYSHQLNLYWVCF 480
 DB 421 KYVESQYNDQDDEASTQTYDSKRNVAWSIDQLPETTDEPLEKGYSHQLNLYWVCF 480
 QY 481 MGSRGITPVLTHKSVDFNMIDSKITQLPVKAYKLGASVAGPFTGGDIQC 540
 DB 481 MGSRGITPVLTHKSVDFNMIDSKITQLPVKAYKLGASVAGPFTGGDIQC 540
 QY 541 TENGSAATITVTPDVYSQKRYARIRHYASTSQITFTLSLDGAPFNOYFEDKTIKNGDILT 600
 DB 541 TENGSAATITVTPDVYSQKRYARIRHYASTSQITFTLSLDGAPFNOYFEDKTIKNGDILT 600
 QY 601 YNSFNLASFSTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSTPEELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 15
 AAW34828
 ID AAW34828 standard; Protein: 644 AA.
 AC AAW34828;
 XX 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein V448A.
 XX
 KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 448

FT /label= V448A
 /note= "wild type Val replaced with Ala"
 XX US5659123-A.
 PN 19-AUG-1997.
 XX 26-AUG-1994: 94US-0295060.
 XX 26-AUG-1994: 94US-0295060.
 XX (PLB2) PLANT GENETIC SYSTEMS NV.
 PA Janssens S, Peferoen M, Van Rie J;
 PI MPI; 1997-424316/39.
 DR Modified Bacillus thuringiensis CryIII proteins - with increased
 XX toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 XX Example 1; Page -: 22pp; English.
 PS
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 11.52 microgram per millilitre, compared to 4.04 microgram per
 CC mlilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 XX
 SQ Sequence 644 AA:
 Query Match 99.9%; Score 3402; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 3.5e-268;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNPNNSEHDTIKTTENNEPTNHNVOYPLAETNPPTLEDLNKKEFLRMADNNTTEALDSS 60
 DB 1 MNPNNSEHDTIKTTENNEPTNHNVOYPLAETNPPTLEDLNKKEFLRMADNNTTEALDSS 60
 QY 61 TTKDVIQKGISVVDLLGVVGFPGALVSFTYNFLNTIMPSEDPWAKAFMEQVEALMDQK 120
 DB 61 TTKDVIQKGISVVDLLGVVGFPGALVSFTYNFLNTIMPSEDPWAKAFMEQVEALMDQK 120
 QY 121 IADYANKKALAEQGLQNNVEDYVSLSSMOKNPVSSRNPHSOGRIRELFSQAESHFRRNS 180
 DB 121 IADYANKKALAEQGLQNNVEDYVSLSSMOKNPVSSRNPHSOGRIRELFSQAESHFRRNS 180
 QY 181 MPSEFASGYEVLEFLTYAQAANTHFLDKDAQIYGEEMGYEKEDIAEFYKROLKLTQEXT 240
 DB 181 MPSEFASGYEVLEFLTYAQAANTHFLDKDAQIYGEEMGYEKEDIAEFYKROLKLTQEXT 240
 QY 241 DHCVKMYNNGDLKRGSSSYESWVNFNRYRREMTLVLDLIALFPLYDVRLYPREVKTELT 300
 DB 241 DHCVKMYNNGDLKRGSSSYESWVNFNRYRREMTLVLDLIALFPLYDVRLYPREVKTELT 300
 QY 301 RDVLTDPYIGVNNLRGXTTESNIENYIKRPHLDYLRHQHTRFQPGYIGNDSEFNYS 360
 DB 301 RDVLTDPYIGVNNLRGXTTESNIENYIKRPHLDYLRHQHTRFQPGYIGNDSEFNYS 360
 QY 361 GNVSTRPSIGSNDITTSFYGKSSSEPYQNLFEENGKEYRAVANTNLAWPSAVYSGVT 420
 DB 361 GNVSTRPSIGSNDITTSFYGKSSSEPYQNLFEENGKEYRAVANTNLAWPSAVYSGVT 420

DB 361 GNVSTRPSIGSNDITTSFYGKSSSEPYQNLFEENGKEYRAVANTNLAWPSAVYSGVT 420
 QY 421 KYEFSQYNDQTEASQOTYDSKRNVGAVSMDSIDQLPETTDEPLEKYSQNLAVMKFL 480
 DB 421 KYEFSQYNDQTEASQOTYDSKRNVGAVSMDSIDQLPETTDEPLEKYSQNLAVMKFL 480
 QY 481 MGSRGITPVLWTNKSVPFFNMIDSKKITQPLVKAYKLGASVAVGAPRTGGDIQC 540
 DB 481 MGSRGITPVLWTNKSVPFFNMIDSKKITQPLVKAYKLGASVAVGAPRTGGDIQC 540
 QY 541 TENGSAATYVTPDVYSQKYPARIRHASTSQITFTLLSDGAPFNQYFEDKTINKGDTLT 600
 DB 541 TENGSAATYVTPDVYSQKYPARIRHASTSQITFTLLSDGAPFNQYFEDKTINKGDTLT 600
 QY 601 YNSFNLSFSTPELGSNNLQIGVGLSGDKVYIDKITEFIPVN 644
 DB 601 YNSFNLSFSTPELGSNNLQIGVGLSGDKVYIDKITEFIPVN 644

Search completed: January 10, 2003, 11:06:28
 Job time : 41 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:05:49 ; Search time 16 Seconds

(without alignments)
1184.273 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406
Sequence: 1 MNPNNRSEHDITKTEENNEV.....TGLSAGDKYIDKIEFIPVN 644

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	644	1 US-07-828-788A-4	Sequence 4, Appl
2	3406	100.0	644	1 US-08-072-281-2	Sequence 2, Appl
3	3406	100.0	644	1 US-08-293-060-2	Sequence 2, Appl
4	3406	100.0	644	1 US-08-759-446-2	Sequence 2, Appl
5	3406	100.0	644	4 US-09-027-998A-2	Sequence 2, Appl
6	3406	100.0	644	5 PCT-US92-11337-4	Sequence 4, Appl
7	3406	100.0	652	3 US-08-996-441B-113	Sequence 113, App
8	3406	100.0	652	3 US-08-993-722A-113	Sequence 113, App
9	3406	100.0	652	3 US-08-993-170A-113	Sequence 113, App
10	3406	100.0	652	3 US-08-993-775B-113	Sequence 113, App
11	3328	97.7	645	1 US-08-295-060-4	Sequence 4, Appl
12	3149	92.5	597	1 US-08-704-966-2	Sequence 2, Appl
13	3149	92.5	597	1 US-08-704-966-2	Sequence 2, Appl
14	3144	92.3	610	3 US-08-704-966-4	Sequence 4, Appl
15	3144	92.3	610	3 US-08-705-438-4	Sequence 4, Appl
16	2564.5	75.3	649	3 US-08-996-441B-109	Sequence 109, App
17	2564.5	75.3	649	3 US-08-993-722A-109	Sequence 109, App
18	2564.5	75.3	649	3 US-08-993-170A-109	Sequence 109, App
19	2564.5	75.3	649	3 US-08-993-775B-109	Sequence 109, App
20	2383	70.0	651	3 US-08-996-441B-56	Sequence 56, Appl
21	2383	70.0	651	3 US-08-993-722A-56	Sequence 56, Appl
22	2383	70.0	651	3 US-08-993-170A-56	Sequence 56, Appl
23	2383	70.0	651	3 US-08-993-775B-56	Sequence 56, Appl
24	2378.5	69.8	652	3 US-08-996-441B-50	Sequence 50, Appl
25	2378.5	69.8	652	3 US-08-993-722A-50	Sequence 50, Appl
26	2378.5	69.8	652	3 US-08-993-170A-50	Sequence 50, Appl
27	2378.5	69.8	652	3 US-08-993-775B-50	Sequence 50, Appl

28	2369.5	69.6	652	3 US-08-996-441B-46	Sequence 46, Appl
29	2369.5	69.6	652	3 US-08-993-722A-46	Sequence 46, Appl
30	2369.5	69.6	652	3 US-08-993-170A-46	Sequence 46, Appl
31	2369.5	69.6	652	3 US-08-993-775B-46	Sequence 46, Appl
32	2355	69.1	651	3 US-08-996-441B-52	Sequence 52, Appl
33	2355	69.1	651	3 US-08-993-722A-52	Sequence 52, Appl
34	2355	69.1	651	3 US-08-993-170A-52	Sequence 52, Appl
35	2355	69.1	651	3 US-08-993-775B-52	Sequence 52, Appl
36	2350.5	69.0	652	3 US-08-996-441B-48	Sequence 48, Appl
37	2350.5	69.0	652	3 US-08-993-722A-48	Sequence 48, Appl
38	2350.5	69.0	652	3 US-08-993-170A-48	Sequence 48, Appl
39	2350.5	69.0	652	3 US-08-993-775B-48	Sequence 48, Appl
40	2349.5	69.0	652	3 US-08-996-441B-54	Sequence 54, Appl
41	2349.5	69.0	652	3 US-08-993-722A-54	Sequence 54, Appl
42	2349.5	69.0	652	3 US-08-993-170A-54	Sequence 54, Appl
43	2349.5	69.0	652	3 US-08-993-775B-54	Sequence 54, Appl
44	2348.5	69.0	652	3 US-08-996-441B-44	Sequence 44, Appl
45	2348.5	69.0	652	3 US-08-993-722A-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-07-828-788A-4
; Sequence 4, Application US/07828788A
; Patent No. 5273746
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRATERA PESTIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESS: DAVID R. SALIMANCHIK
; STREET: 2421 N.W. 41ST STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,788A
; FILING DATE: 19920129
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIMANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 644 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: NIGRIENSIS
; INDIVIDUAL ISOLATE: PS40D1
; IMMEDIATE SOURCE:
; LIBRARY: LAMDADEM (TM) - 11 LIBRARY OF FRANK GAERTNER
; CLONE: 40D1
; US-07-828-788A-4

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPNNRSEHDITKTENNENVPNNVQYPLAETPNPTLEDINKEFLRMADNTEALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNNVQYPLAETPNPTLEDINKEFLRMADNTEALDSS 60
QY 61 TTKVDIYGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
DB 61 TTKVDIYGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQASHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQASHFRNS 180
QY 181 MPSAISGVEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIABFYKROLKLTQERYT 240
DB 181 MPSAISGVEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIABFYKROLKLTQERYT 240
QY 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
DB 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
QY 301 RDVLTDPVGVNMLRGYGTFSNIENYIRKPHLEFDYLHRIQFHTRFQPGYGNDSFNWMS 360
DB 301 RDVLTDPVGVNMLRGYGTFSNIENYIRKPHLEFDYLHRIQFHTRFQPGYGNDSFNWMS 360
QY 361 GNYVSTRPSISGNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVSGLT 420
DB 361 GNYVSTRPSISGNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVSGLT 420
QY 421 KYVESQYNDQDEASTQYDSKRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCEL 480
DB 421 KYVESQYNDQDEASTQYDSKRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCEL 480
QY 481 MGSRGITPVLTWTHKSVDFNMDSKKITQULPLVAYKLGASAVAGPRTGGDIIOC 540
DB 481 MGSRGITPVLTWTHKSVDFNMDSKKITQULPLVAYKLGASAVAGPRTGGDIIOC 540
QY 541 TENGSAATIVTPDVYSQKYRARIHYASTQSITFTLSLDGAPFNQYEDKTIKNGDTLT 600
DB 541 TENGSAATIVTPDVYSQKYRARIHYASTQSITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIPIVN 644
DB 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIPIVN 644

```

RESULT 2

US-08-072-281-2
 : Sequence 2, Application US/08072281
 : Patent No. 5495071
 : GENERAL INFORMATION:
 : APPLICANT: Fischhoff, David A.
 : APPLICANT: Fuchs, Roy L.
 : APPLICANT: Lawrik, Paul B.
 : APPLICANT: McPherson, Sylvia A.
 : APPLICANT: Perlak, Frederick J.
 : TITLE OF INVENTION: Insect Resistant Plants
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lawrence M. Lavin, Jr., Monsanto Co., BB4F
 : STREET: 700 Chesterfield Parkway No. 5495071th
 : CITY: St. Louis
 : STATE: Missouri
 : COUNTRY: United States of America
 : ZIP: 63198
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/072,281
 : FILING DATE: 19930604
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/523284
 : FILING DATE: 14-MAY-1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lavin Jr., Lawrence M.
 : REGISTRATION NUMBER: 30,768
 : REFERENCE/DOCKET NUMBER: 38-21(10629)A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (314) 537-7286
 : TELEFAX: (314) 537-6047
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 644 amino acids
 : TYPE: AMINO ACID
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 :
 : US-08-072-281-2

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPNNRSEHDITKTENNENVPNNVQYPLAETPNPTLEDINKEFLRMADNTEALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNNVQYPLAETPNPTLEDINKEFLRMADNTEALDSS 60
QY 61 TTKVDIYGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
DB 61 TTKVDIYGISVGDLLGVGPFPGALVSFTYNEFLNTIMPSDEPMKAFMEQVLEALDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQASHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRELFSQASHFRNS 180
QY 181 MPSAISGVEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIABFYKROLKLTQERYT 240
DB 181 MPSAISGVEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIABFYKROLKLTQERYT 240
QY 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
DB 241 DHCVMYVNGDLKLGSSYESWVNFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
QY 301 RDVLTDPVGVNMLRGYGTFSNIENYIRKPHLEFDYLHRIQFHTRFQPGYGNDSFNWMS 360
DB 301 RDVLTDPVGVNMLRGYGTFSNIENYIRKPHLEFDYLHRIQFHTRFQPGYGNDSFNWMS 360
QY 361 GNYVSTRPSISGNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVSGLT 420
DB 361 GNYVSTRPSISGNDIITSPFYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVSGLT 420
QY 421 KYVESQYNDQDEASTQYDSKRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCEL 480
DB 421 KYVESQYNDQDEASTQYDSKRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLNYMCEL 480
QY 481 MGSRGITPVLTWTHKSVDFNMDSKKITQULPLVAYKLGASAVAGPRTGGDIIOC 540
DB 481 MGSRGITPVLTWTHKSVDFNMDSKKITQULPLVAYKLGASAVAGPRTGGDIIOC 540
QY 541 TENGSAATIVTPDVYSQKYRARIHYASTQSITFTLSLDGAPFNQYEDKTIKNGDTLT 600
DB 541 TENGSAATIVTPDVYSQKYRARIHYASTQSITFTLSLDGAPFNQYEDKTIKNGDTLT 600
QY 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIPIVN 644
DB 601 YNSFNLASSTPELSSGNLQIGVTGLSAGDKYIDKIEFIPIVN 644

```

RESULT 3

US-08-295-060-2
 : Sequence 2, Application US/08295060
 : Patent No. 5659123
 : GENERAL INFORMATION:
 : APPLICANT: VAN RIE, Jeroen
 : APPLICANT: JANSSEN, Stefan
 : APPLICANT: PERFEROEN, Marinix
 : TITLE OF INVENTION: NEW DIABROTICA TOXINS
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Burns, Doane, Swecker & Malchis
 : STREET: P.O. Box 1404
 : CITY: Alexandria
 : STATE: Virginia
 : COUNTRY: United States
 : ZIP: 22313-1404
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/295,060
 : FILING DATE: 26-AUG-1994
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Crane-Feurly, Sharon E
 : REGISTRATION NUMBER: 36,113
 : REFERENCE/DOCKET NUMBER: 010830-052
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 836-6620
 : TELEFAX: (703) 836-6620
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 644 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-295-060-2

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7,1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTYKEFLRMADNTEALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTYKEFLRMADNTEALDSS 60
 QY 61 TTKVYIOKGISVVDLLGVGFPFGALVSYTFNPLTIPSEDPKAFMEQVEALMDOK 120
 DB 61 TTKVYIOKGISVVDLLGVGFPFGALVSYTFNPLTIPSEDPKAFMEQVEALMDOK 120
 QY 121 IADYAKKALAELOGLNVEDYSAISSMOKNPVSSRNPHSOGRIEELSQAESHFRNS 180
 DB 121 IADYAKKALAELOGLNVEDYSAISSMOKNPVSSRNPHSOGRIEELSQAESHFRNS 180
 QY 181 MPFAISGEYVLFYTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLTQOET 240
 DB 181 MPFAISGEYVLFYTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLTQOET 240
 QY 241 DHCVKWTNVGLDKLGGSSYEWVFNRYRRMTLTVDLALFPLVYRRLPKVEKTELT 300
 DB 241 DHCVKWTNVGLDKLGGSSYEWVFNRYRRMTLTVDLALFPLVYRRLPKVEKTELT 300
 QY 301 RDVLTDPVGVNRLRGYGTSTSENTYIRKPHLFDYLRHIOFHRFOPGYGNDSPYWS 360
 DB 301 RDVLTDPVGVNRLRGYGTSTSENTYIRKPHLFDYLRHIOFHRFOPGYGNDSPYWS 360
 QY 361 GNYSTRSISGNDITSPFYGNKSSPEVQNLIEFNGEKYRAVANTNLAVPSSVYSGVT 420
 DB 361 GNYSTRSISGNDITSPFYGNKSSPEVQNLIEFNGEKYRAVANTNLAVPSSVYSGVT 420
 QY 421 KVESQYNDQIDEASTQYTDKRNKAVSWDSIDQLPETTDEPLEKCYSHQNLVWCFL 480

US-08-759-446-2
 : Sequence 2, Application US/08759446
 : Patent No. 5763241
 : GENERAL INFORMATION:
 : APPLICANT: Fischhoff, David A.
 : APPLICANT: Fuchs, Roy L.
 : APPLICANT: Lavrik, Paul B.
 : APPLICANT: McPherson, Sylvia A.
 : APPLICANT: Perlak, Frederick J.
 : TITLE OF INVENTION: Insect Resistant Plants
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lawrence M. Lavlin, Jr., Monsanto Co., BBAF
 : STREET: 700 Chesterfield Parkway No. 5763241ch
 : CITY: St. Louis
 : STATE: Missouri
 : COUNTRY: United States of America
 : ZIP: 63198
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/759,446
 : FILING DATE: 05-DEC-1996
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/072,281
 : FILING DATE:
 : APPLICATION NUMBER: US 07/523284
 : FILING DATE: 14-MAY-1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lavlin Jr., Lawrence M.
 : REGISTRATION NUMBER: 30,768
 : REFERENCE/DOCKET NUMBER: 38-21(10629)A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (314) 537-7286
 : TELEFAX: (314) 537-6047
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 644 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-759-446-2

Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 7,1e-277;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTYKEFLRMADNTEALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTYKEFLRMADNTEALDSS 60
 QY 61 TTKVYIOKGISVVDLLGVGFPFGALVSYTFNPLTIPSEDPKAFMEQVEALMDOK 120

```

: SEQUENCE CHARACTERISTICS:
: LENGTH: 644 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: US-09-027-998A-2

Query Match      100.0%; Score 3406; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 7.1e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 MNPNRSEHDITKTENNEVEPTNNHQYLAETPMPTELDNLYKDFLRNTADNNTAIDSS 60
Db 1 MNPNRSEHDITKTENNEVEPTNNHQYLAETPMPTELDNLYKDFLRNTADNNTAIDSS 60

QY 61 TTKDYIQGISVGGDLGCVGFPFGGALVSFTYFNLNTIMPSSEDPMKAFMEQYBALDOK 120
Db 61 TTKDYIQGISVGGDLGCVGFPFGGALVSFTYFNLNTIMPSSEDPMKAFMEQYBALDOK 120

QY 121 IADYAKNALAELOGIQNNVEDYSAISSWQKNVSSNHPSSQRIEELSQAASHRRNS 180
Db 121 IADYAKNALAELOGIQNNVEDYSAISSWQKNVSSNHPSSQRIEELSQAASHRRNS 180

QY 181 MPFASISGEVLFITTYAQAAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKTQEYT 240
Db 181 MPFASISGEVLFITTYAQAAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKTQEYT 240

QY 241 DHCYKMYVWGDLKRGSSYESWMEFNRYRREMTLTIVDLTAFLPYVRRLYKREVKTELT 300
Db 241 DHCYKMYVWGDLKRGSSYESWMEFNRYRREMTLTIVDLTAFLPYVRRLYKREVKTELT 300

QY 301 RDVLTPDIVGVNNLRGXYGTFPSNTENYIRKPHLEFDLHRIQFHTRFQPGYGGNDSFNWYS 360
Db 301 RDVLTPDIVGVNNLRGXYGTFPSNTENYIRKPHLEFDLHRIQFHTRFQPGYGGNDSFNWYS 360

QY 361 GNYSTPRSTGSNDLITSPFGKSSSRPQNLFENGKRYRAVANTMLAWPSAVSYSGVT 420
Db 361 GNYSTPRSTGSNDLITSPFGKSSSRPQNLFENGKRYRAVANTMLAWPSAVSYSGVT 420

QY 421 KYEFSQYNDQDEASTQTYDSKRNVGAVSMDSIDQLPETTDEBLEKGYSHQNTYVWCF 480
Db 421 KYEFSQYNDQDEASTQTYDSKRNVGAVSMDSIDQLPETTDEBLEKGYSHQNTYVWCF 480

QY 481 MGSRGITPVLTWYHKSVDFPNMIDSKKITQLPLVKAAYKLQSGASVYAGFRPMGGDIQC 540
Db 481 MGSRGITPVLTWYHKSVDFPNMIDSKKITQLPLVKAAYKLQSGASVYAGFRPMGGDIQC 540

QY 541 TENSSAATIVTPDVYSQKYRARIRIHASTSQTFTLSLGAFFNOYFPPKTTNKGDITL 600
Db 541 TENSSAATIVTPDVYSQKYRARIRIHASTSQTFTLSLGAFFNOYFPPKTTNKGDITL 600

QY 601 YNSFNLASFSTPELSGNNLIQIGVTLGSAGDKVYIDKIEFIPVN 644
Db 601 YNSFNLASFSTPELSGNNLIQIGVTLGSAGDKVYIDKIEFIPVN 644

RESULT 6
PCT-US92-11337-4
: Sequence 4, Application PC/TUS9211337
: GENERAL INFORMATION:
: APPLICANT: PAYNE, JEWEL M.
: APPLICANT: HICKLE, LESLIE A.
: TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
: TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID R. SALIMANCHIK
: STREET: 2421 N.W. 41st STREET, SUITE A-1
: CITY: GAINESVILLE
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:

```

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337
FILING DATE: 19921231
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SALIVANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGERIENSIS
INDIVIDUAL ISOLATE: PS40D1
IMMEDIATE SOURCE:
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF FRANK GAERTNER
CLONE: 40D1
PCT-US92-11337-4

Query Match          100.0%: Score 3406; DB 5; Length 644:
Best Local Similarity 100.0%: Pred. No. 7.1e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNEPTNHVOYPLAETPNPTLEDNTKEFLRMTADNNTLEALDSS 60
DB 1 MNPNNSEHDTIKTTENNEPTNHVOYPLAETPNPTLEDNTKEFLRMTADNNTLEALDSS 60
QY 61 TTKDVIOKGSIVGDLGVGFPFGALVSFTYNFTLNTIMPSEDPMKAFMEOVEALMDOK 120
DB 61 TTKDVIOKGSIVGDLGVGFPFGALVSFTYNFTLNTIMPSEDPMKAFMEOVEALMDOK 120
QY 121 IADYAKKALAELOGLONNVEDYVSALSWQKNPVSSRNPHSGRIRELFSAESHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSWQKNPVSSRNPHSGRIRELFSAESHFRNS 180
QY 181 MPFAISGVEYLFYTYAQAANPHLFLKPAQIAGEEMGEEKEDIAEFYRQKLIOEYT 240
DB 181 MPFAISGVEYLFYTYAQAANPHLFLKPAQIAGEEMGEEKEDIAEFYRQKLIOEYT 240
QY 241 DHCKWYNVGLDKLGRSSYSWVFNRYRREMTLTVLDLALPELVDRVLPKREKTELT 300
DB 241 DHCKWYNVGLDKLGRSSYSWVFNRYRREMTLTVLDLALPELVDRVLPKREKTELT 300
QY 301 RDVLTDPVGNVNLRGYGTFTSNIENYIRKPHLDYLRHQFHTREPOGYGNDSEFYMS 360
DB 301 RDVLTDPVGNVNLRGYGTFTSNIENYIRKPHLDYLRHQFHTREPOGYGNDSEFYMS 360
QY 361 GNYSTRPSIGSNDIITSPFGKNSSEPVONLEFNGEKYVAAVANTMLAVWPSAVYSGVT 420
DB 361 GNYSTRPSIGSNDIITSPFGKNSSEPVONLEFNGEKYVAAVANTMLAVWPSAVYSGVT 420
QY 421 KVEFSQYNDQDEASTQTYDSKRNAGVSWDSIDQLPEPTTDEPLEKGYSHQNLVWCFEL 480
DB 421 KVEFSQYNDQDEASTQTYDSKRNAGVSWDSIDQLPEPTTDEPLEKGYSHQNLVWCFEL 480
QY 481 MGSNGTIPVLTWTHKSVDFENMIDSKKITQPLPYKAYKLGSGASVAVGPFRTGSDIIC 540

```

```

DB 481 MGSNGTIPVLTWTHKSVDFENMIDSKKITQPLPYKAYKLGSGASVAVGPFRTGSDIIC 540
QY 541 TENSANATVYTPVVSQKRIARHYASTSOIFETLSLGDAPPNOYFPKTIKGTTLT 600
DB 541 TENSANATVYTPVVSQKRIARHYASTSOIFETLSLGDAPPNOYFPKTIKGTTLT 600
QY 601 YNSFNIASTPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNIASTPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644

RESULT 7
US-08-996-441B-113
Sequence 113, Application US/08996441B
Patent No. 6023013
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brusock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
APPLICANT: Romano, Charles
TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-996-441B-113

Query Match          100.0%: Score 3406; DB 3; Length 652:
Best Local Similarity 100.0%: Pred. No. 7.2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNEPTNHVOYPLAETPNPTLEDNTKEFLRMTADNNTLEALDSS 60
DB 9 MNPNNSEHDTIKTTENNEPTNHVOYPLAETPNPTLEDNTKEFLRMTADNNTLEALDSS 68
QY 61 TTKDVIOKGSIVGDLGVGFPFGALVSFTYNFTLNTIMPSEDPMKAFMEOVEALMDOK 120
DB 61 TTKDVIOKGSIVGDLGVGFPFGALVSFTYNFTLNTIMPSEDPMKAFMEOVEALMDOK 128
QY 121 IADYAKKALAELOGLONNVEDYVSALSWQKNPVSSRNPHSGRIRELFSAESHFRNS 180

```



```

Db 129 IADYAKKALAELOGLONNVEDYVSSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 188
QY 181 MPSFAISGYEVLFTTYAQAANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOERYT 240
Db 189 MPSFAISGYEVLFTTYAQAANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOERYT 248
QY 241 DHCVKWYVGLDLKRGSSVSESWVNFNRKRYREMTLVLDLALFPLDVRILYPREVTELT 300
Db 249 DHCVKWYVGLDLKRGSSVSESWVNFNRKRYREMTLVLDLALFPLDVRILYPREVTELT 308
QY 301 RDVLTDPYGVNNLRGCTTFPSNIENYIRKPHLFDYLRHIOFHTRPOGYGNDSEFNYS 360
Db 309 RDVLTDPYGVNNLRGCTTFPSNIENYIRKPHLFDYLRHIOFHTRPOGYGNDSEFNYS 368
QY 361 GNVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Db 369 GNVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANINLAWPSAVYSGVT 428
QY 421 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
Db 429 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 488
QY 481 MGSRGITPVLTHKSVDFNMIDSKKITQPLVKAYKLGASVAVAGPRTGGDIIOC 540
Db 489 MGSRGITPVLTHKSVDFNMIDSKKITQPLVKAYKLGASVAVAGPRTGGDIIOC 548
QY 541 TENGSAATIVTPDVYSQYKRYARIHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 600
Db 549 TENGSAATIVTPDVYSQYKRYARIHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 608
QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 644
Db 609 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 652

```

RESULT 8

US-08-993-722A-113

Sequence 113, Application US/08993722A

Patent No. 6060594

GENERAL INFORMATION:

```

APPLICANT: English, Leigh H.
APPLICANT: Brusock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

```

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-722A-113

```

```

Query Match 100.0%; Score 3406; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 7, 2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNPNRSEHDITKTENNEVPTNNVOYPLATPMTLEDLNYKFLMTADNNTALDSS 60
Db 9 MNPNRSEHDITKTENNEVPTNNVOYPLATPMTLEDLNYKFLMTADNNTALDSS 68
QY 61 TTKDVIQGISVVDLLGVGFPGALVSPYTNFLMTIMPSDEPMKAFMEQVEALMDOK 120
Db 69 TTKDVIQGISVVDLLGVGFPGALVSPYTNFLMTIMPSDEPMKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLONNVEDYVSSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
Db 129 IADYAKKALAELOGLONNVEDYVSSALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 188
QY 181 MPSFAISGYEVLFTTYAQAANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOERYT 240
Db 189 MPSFAISGYEVLFTTYAQAANTHFLFKDAQIYGEEMGEKEDIAEFYKROKLQOERYT 248
QY 241 DHCVKWYVGLDLKRGSSVSESWVNFNRKRYREMTLVLDLALFPLDVRILYPREVTELT 300
Db 249 DHCVKWYVGLDLKRGSSVSESWVNFNRKRYREMTLVLDLALFPLDVRILYPREVTELT 308
QY 301 RDVLTDPYGVNNLRGCTTFPSNIENYIRKPHLFDYLRHIOFHTRPOGYGNDSEFNYS 360
Db 309 RDVLTDPYGVNNLRGCTTFPSNIENYIRKPHLFDYLRHIOFHTRPOGYGNDSEFNYS 368
QY 361 GNVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Db 369 GNVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANINLAWPSAVYSGVT 428
QY 421 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
Db 429 KVEFSQYNDQTDASTQYDYSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 488
QY 481 MGSRGITPVLTHKSVDFNMIDSKKITQPLVKAYKLGASVAVAGPRTGGDIIOC 540
Db 489 MGSRGITPVLTHKSVDFNMIDSKKITQPLVKAYKLGASVAVAGPRTGGDIIOC 548
QY 541 TENGSAATIVTPDVYSQYKRYARIHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 600
Db 549 TENGSAATIVTPDVYSQYKRYARIHYASTSQITFTLSDGAPFNQYFDTINKGDTLT 608
QY 601 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 644
Db 609 YNSFNLASFTPELSGNNLQIGVTGLSAGDKVYIDKIEFIYVN 652

```

RESULT 9

US-08-993-170A-113

Sequence 113, Application US/08993170A

Patent No. 6063597

GENERAL INFORMATION:

```

APPLICANT: English, Leigh H.
APPLICANT: Brusock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO

```


TITLE OF INVENTION: COLEOPTERAN INSECTS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.170A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-170A-113

Query Match 100.0%; Score 3406; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 7.2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTITKTENNEVPYTHVOYPLAETPNPTELDLNTKEFLRMADNNTALDSS 60
DB 9 MNPNNSEHDTITKTENNEVPYTHVOYPLAETPNPTELDLNTKEFLRMADNNTALDSS 68
QY 61 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTLNTIPSDPKAFMEQVEALMDOK 120
DB 69 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTLNTIPSDPKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRIREFLSQAESHFRNS 180
DB 129 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRIREFLSQAESHFRNS 188
QY 181 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240
DB 189 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 248
QY 241 DHCKYKYNVGLDKRGSSYSWVAFNRYRREMTITVDLALPPLVDVRLYPEKVEKTELT 300
DB 249 DHCKYKYNVGLDKRGSSYSWVAFNRYRREMTITVDLALPPLVDVRLYPEKVEKTELT 308
QY 301 RDVLTIDYVGNLNGYGTFSNIENYIRKPHLEFDYLRHQFHTRFQPGYTGNDSEFNWMS 360
DB 309 RDVLTIDYVGNLNGYGTFSNIENYIRKPHLEFDYLRHQFHTRFQPGYTGNDSEFNWMS 368
QY 361 GNYVSTRPISGSDIITSFYGNKSSPVPONLEFNGEKYYRAVANIMLAWPMSAVYSGVT 420
DB 369 GNYVSTRPISGSDIITSFYGNKSSPVPONLEFNGEKYYRAVANIMLAWPMSAVYSGVT 428
QY 421 KVESQVQNDQDEASTQTYOSKRVAGVAMSDSIDQLPETTDEPLEKGYSHQLWYVACFL 480
DB 429 KVESQVQNDQDEASTQTYOSKRVAGVAMSDSIDQLPETTDEPLEKGYSHQLWYVACFL 488
QY 481 MGSRGITPVLWTJHKSVDFFNMIDSKKITQPLVKAYKLOSASVYVAGPRTGGDITQC 540
DB 489 MGSRGITPVLWTJHKSVDFFNMIDSKKITQPLVKAYKLOSASVYVAGPRTGGDITQC 548

QY 541 TENGSAATIVYTPDVSYSQKRYARIHYASTSQITFTLSDGAPPNOYFDPKTIKNGDTLT 600
DB 549 TENGSAATIVYTPDVSYSQKRYARIHYASTSQITFTLSDGAPPNOYFDPKTIKNGDTLT 608
QY 601 YNSFNILASFSTPELSCNNLQIGVTGLSAGDKYIDIEFIPVN 644
DB 609 YNSFNILASFSTPELSCNNLQIGVTGLSAGDKYIDIEFIPVN 652

RESULT 10
US-08-993-775B-113
Sequence 113, Application US/08993775B
Patent No. 6077824
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brunsack, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terach, Michael A.
TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.775B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-775B-113

Query Match 100.0%; Score 3406; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 7.2e-277;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTITKTENNEVPYTHVOYPLAETPNPTELDLNTKEFLRMADNNTALDSS 60
DB 9 MNPNNSEHDTITKTENNEVPYTHVOYPLAETPNPTELDLNTKEFLRMADNNTALDSS 68
QY 61 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTLNTIPSDPKAFMEQVEALMDOK 120
DB 69 TTYDVIOKGISVVDLGVGFFPGALVSFTYNTLNTIPSDPKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRIREFLSQAESHFRNS 180
DB 129 IADYAKKALAELOGLQNNVEDYVSLSSQKPNVSSRNPHSGRIREFLSQAESHFRNS 188
QY 181 MPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240

```

Db 189 MPEFALSGVEVLFPTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKTOEY 248
QY 241 DHCWYNNVGLDKLRGSSYESWVNNRNRREMTLVLDLIALFPLDYVLYKREYKTELT 300
Db 249 DHCWYNNVGLDKLRGSSYESWVNNRNRREMTLVLDLIALFPLDYVLYKREYKTELT 308
QY 301 RDVLTDPYGVNNLRGYGTTFNSIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 360
Db 309 RDVLTDPYGVNNLRGYGTTFNSIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 368
QY 361 GNVSTRPSIGSNDITTFPGYKSEEPQNLFEENGEKYRAVANTNLAVMPSAYSGVT 420
Db 369 GNVSTRPSIGSNDITTFPGYKSEEPQNLFEENGEKYRAVANTNLAVMPSAYSGVT 428
QY 421 KVEFSQNDQDEASTQYDSKRNMGAVSMDSIDOLPEPTDEPLEKGYSHOANTVMCFL 480
Db 429 KVEFSQNDQDEASTQYDSKRNMGAVSMDSIDOLPEPTDEPLEKGYSHOANTVMCFL 488
QY 481 MGSRGRTIVLWTHKSVDFNNMIDSKITPOLPVKAYKLGASVAVAGPFTGGDIIOC 540
Db 489 MGSRGRTIVLWTHKSVDFNNMIDSKITPOLPVKAYKLGASVAVAGPFTGGDIIOC 548
QY 541 TENGSAATIVYTPDVYSQKRYARHIASTQITFTLSLDGAPFNOYFDDKTKNGDTLT 600
Db 549 TENGSAATIVYTPDVYSQKRYARHIASTQITFTLSLDGAPFNOYFDDKTKNGDTLT 608
QY 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 609 YNSFNLASFTPELSCNNLQIGVTGLSAGDKVYIDKIEFIPVN 652

```

RESULT 11

US-08-295-060-4

```

; Sequence 4, Application US/08295060
; Patent No. 5659123
; GENERAL INFORMATION:
; APPLICANT: VAN RIE, Jerroen
; APPLICANT: JANSSENS, Stefan
; APPLICANT: PERFEROEN, Marilix
; TITLE OF INVENTION: NEW DIABROTICA TOXINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,060
; FILING DATE: 26-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; US-08-295-060-4

```

Query Match 97.7%; Score 3328; DB 1; Length 645;
 Best Local Similarity 98.6%; Pred. No. 2,4e-270;
 Matches 634; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

QY 2 NPNNSSEHDITKTEBNNVPTNNHVOYPLAETPNPTLEDLANKELRMADNNTALDSSST 61
Db 3 NPNNSSEHDITKTEBNNVPTNNHVOYPLAETPNPTLEDLANKELRMADNNTALDSSST 62
QY 62 TKDVIQKISVVGDLGAVGFPFGALVSFTYNTLNTIWPSEDPWAKAFMEQVEALMDOKI 121
Db 63 TKDVIQKISVVGDLGAVGFPFGALVSFTYNTLNTIWPSEDPWAKAFMEQVEALMDOKI 122
QY 122 ADYAKNKLAELOGLONNVEDYVSAISWQKNPVSSNPNHSGQIRLRELFSQASHFENSM 181
Db 123 ADYAKNKLAELOGLONNVEDYVSAISWQKNPVSSNPNHSGQIRLRELFSQASHFENSM 182
QY 182 PSFAISGYEVLFTTVAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKTOEYTD 241
Db 183 PSFAISGYEVLFTTVAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKTOEYTD 242
QY 242 HCWYNNVGLDKLRGSSYESWVNNRNRREMTLVLDLIALFPLDYVLYKREYKTELT 301
Db 243 HCWYNNVGLDKLRGSSYESWVNNRNRREMTLVLDLIALFPLDYVLYKREYKTELT 302
QY 302 DVLTDPIYGVNNLRGYGTTFNSIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 361
Db 303 DVLTDPIYGVNNLRGYGTTFNSIENYIRKPHLFDYLRHIOFHTRPQCYGNDSEFNWS 362
QY 362 NYVSTRPSIGSNDITTFPGYKSEEPQNLFEENGEKYRAVANTNLAVMPSAYSGVT 421
Db 363 NYVSTRPSIGSNDITTFPGYKSEEPQNLFEENGEKYRAVANTNLAVMPSAYSGVT 422
QY 422 VEFQYNDQDEASTQYDSKRNMGAVSMDSIDOLPEPTDEPLEKGYSHOANTVMCFL 481
Db 423 VEFQYNDQDEASTQYDSKRNMGAVSMDSIDOLPEPTDEPLEKGYSHOANTVMCFL 482
QY 482 QGSRGTIVLWTHKSVDFNNMIDSKITPOLPVKAYKLGASVAVAGPFTGGDIIOC 541
Db 483 QGSRGTIVLWTHKSVDFNNMIDSKITPOLPVKAYKLGASVAVAGPFTGGDIIOC 542
QY 542 ENGSAATIVYTPDVYSQKRYARHIASTQITFTLSLDGAPFNOYFDDKTKNGDTLT 601
Db 543 ENGSAATIVYTPDVYSQKRYARHIASTQITFTLSLDGAPFNOYFDDKTKNGDTLT 602
QY 602 NSFNLASFSTPELSCNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 603 NSFNLASFSTPELSCNNLQIGVTGLSAGDKVYIDKIEFIPVN 645

```

RESULT 12

US-08-704-966-2

```

; Sequence 2, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rochelleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; PC-DOS/MS-DOS

```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,966
FILING DATE: 29-AUG-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,482
FILING DATE: 09-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-966-2

Query Match 92.5%; Score 3149; DB 3; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.1e-255;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALSDSTTKDVYKIGISVVGDLGVGFPFGALVSPYTNFLTITPSEDPMK 107
DB 1 MTADNNTALSDSTTKDVYKIGISVVGDLGVGFPFGALVSPYTNFLTITPSEDPMK 60
QY 108 AFMEQVALMDOKIADYAKKALAELOGIANNVEDYVSALSSWQKNPVSSRNPHSGRIR 167
DB 61 AFMEQVALMDOKIADYAKKALAELOGIANNVEDYVSALSSWQKNPVSSRNPHSGRIR 120
QY 168 ELFSQASHRNSMPSFAISGEYVFLTYTAAANTHLFLKDAQIYGEEMGEKEDIAE 227
DB 121 ELFSQASHRNSMPSFAISGEYVFLTYTAAANTHLFLKDAQIYGEEMGEKEDIAE 180
QY 228 FYKROLKLTQEDYDHCYKMYNVDGLKRGSSYESWVNFNRYRREMTLVLDIALFPLYD 287
DB 181 FYKROLKLTQEDYDHCYKMYNVDGLKRGSSYESWVNFNRYRREMTLVLDIALFPLYD 240
QY 288 VRLPKREKTELTDVLDPLVGVNNLRGTYTNTENTIRKHLDDYLRHIOFHRFQ 347
DB 241 VRLPKREKTELTDVLDPLVGVNNLRGTYTNTENTIRKHLDDYLRHIOFHRFQ 300
QY 348 PGYGNDSFNWMSGNYSYTRPSISNDIITSFYGNKSSEPVQNLFEENGKRYRAVANTN 407
DB 301 PGYGNDSFNWMSGNYSYTRPSISNDIITSFYGNKSSEPVQNLFEENGKRYRAVANTN 360
QY 408 LAVPNSAVYSGVTVERSOYNDOTDEASTQYDYSKRNVGAVSMSTIOQLPPTTDEPLEK 467
DB 361 LAVPNSAVYSGVTVERSOYNDOTDEASTQYDYSKRNVGAVSMSTIOQLPPTTDEPLEK 420
QY 468 GYSQOLNVMCFLMQSGHGTPLVLTWTHKSVDFNMIDSKITQLPLVKAKKLOGSASVY 527
DB 421 GYSQOLNVMCFLMQSGHGTPLVLTWTHKSVDFNMIDSKITQLPLVKAKKLOGSASVY 480
QY 528 AGPRTGDIIOCTENGSAATYYTPDVYSYQKTRARIHVASTQITFTTSLDGAPEYQY 587
DB 481 AGPRTGDIIOCTENGSAATYYTPDVYSYQKTRARIHVASTQITFTTSLDGAPEYQY 540

QY 588 YEDKTINKGDLITNSFNFLASFSTPPELSGNNLOIGVTGLSAGKRYIDKIEFIPV 644
DB 541 YEDKTINKGDLITNSFNFLASFSTPPELSGNNLOIGVTGLSAGKRYIDKIEFIPV 597

RESULT 13
US-08-705-438-2
Sequence 2, Application US/08705438
Patent No. 6015891
GENERAL INFORMATION:
APPLICANT: Adang, Michael J.
APPLICANT: Rochelleau, Thomas A.
APPLICANT: Merlo, Donald
APPLICANT: Murray, Elizabeth E.
TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Sallwanchik, Lloyd & Sallwanchik
STREET: 1000 Legion Place, Suite 1750
CITY: Orlando
STATE: Florida
COUNTRY: USA
ZIP: 32801

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,438
FILING DATE: 29-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,839
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,191
FILING DATE: 03-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,844
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,482
FILING DATE: 09-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-705-438-2

Query Match 92.5%; Score 3149; DB 3; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.1e-255;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALSDSTTKDVYKIGISVVGDLGVGFPFGALVSPYTNFLTITPSEDPMK 107
DB 1 MTADNNTALSDSTTKDVYKIGISVVGDLGVGFPFGALVSPYTNFLTITPSEDPMK 60
QY 108 AFMEQVALMDOKIADYAKKALAELOGIANNVEDYVSALSSWQKNPVSSRNPHSGRIR 167
DB 61 AFMEQVALMDOKIADYAKKALAELOGIANNVEDYVSALSSWQKNPVSSRNPHSGRIR 120

```

?      ATTORNEY/AGENT INFORMATION:
?      NAME: Lloyd, Jeff
?      REGISTRATION NUMBER: 35,589
?      REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 407-426-7500
?      TELEFAX: 407-839-8589
?      INFORMATION FOR SEQ ID NO: 4:
?      SEQUENCE CHARACTERISTICS:
?          LENGTH: 610 amino acids
?          TYPE: amino acid
?          STRANDEDNESS: single
?          TOPOLOGY: linear
?      MOLECULE TYPE: protein
US-08-704-966-4

Query Match          92.3%; Score 3144; DB 3; Length 610;
Best Local Similarity 99.8%; Pred. No. 5,86-255;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY      48 MTADNNTEALDSSTTDVIOKGISVVGDLGVCPPFGALVSTRYNPLNTIMPSEDPMK 107
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       1 MADNNTREALDSSSTDVDVIQKISVAGDLGVCGPFPFGALVSFTYNPLNTIMPSEDPMK 60

QY      108 AFMEQVEALMDKDIADIAVANKKALAEILOGLONNVEDYVALSSWQKNVSSRNPHSGRIR 167
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       61 AFMEQVEALMDKDIADIAVANKKALAEILOGLONNVEDYVALSSWQKNVSSRNPHSGRIR 120

QY      168 ELFSQAESHFRNSMSPFAISGYEVLFITTYAQAANTHLFLLKDAQIYEEMGYEKEDIAE 227
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      121 ELFSQAESHFRNSMSPFAISGYEVLFITTYAQAANTHLFLLKDAQIYEEMGYEKEDIAE 180

```

```

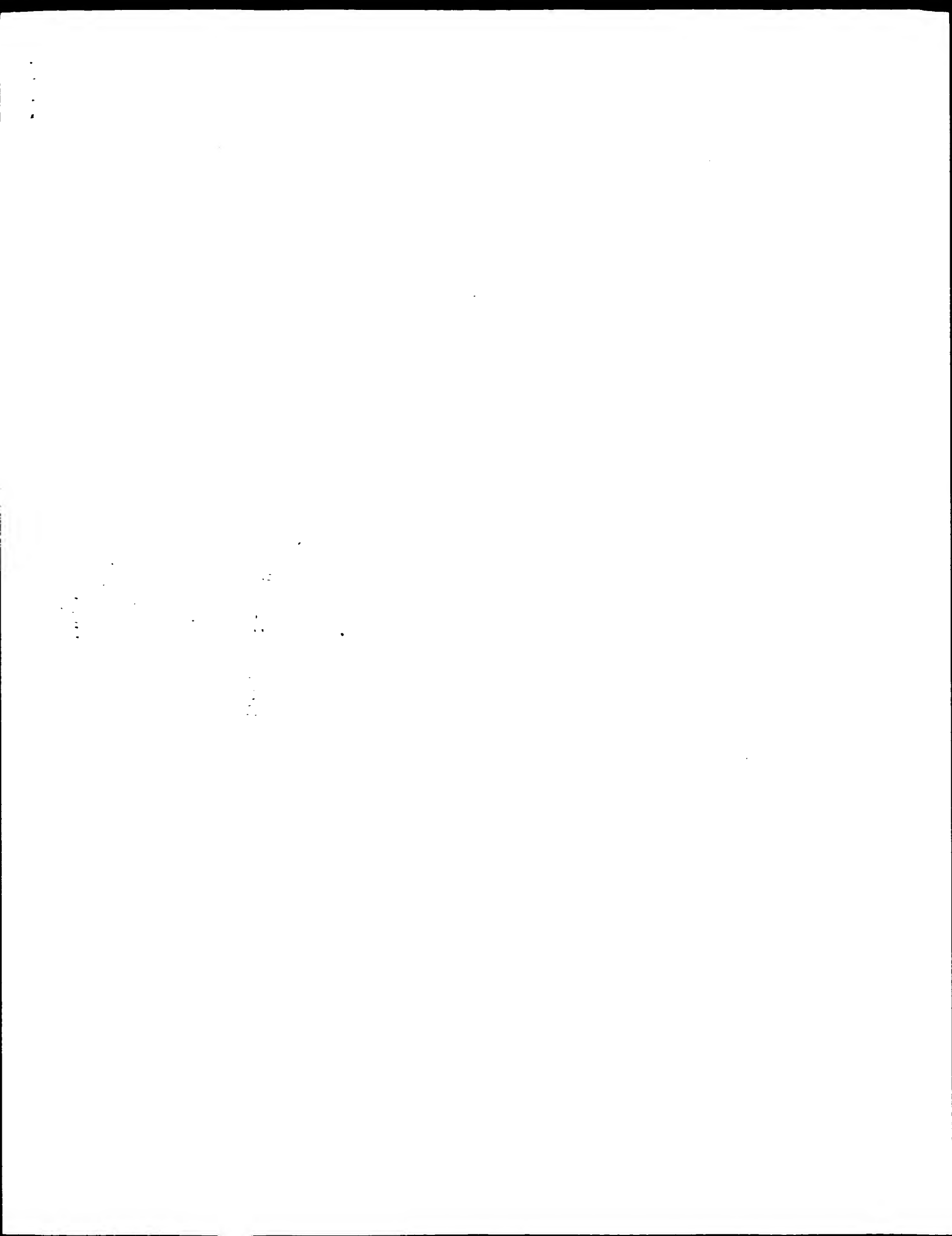
RESULT 15
US-08-705-438-4
/ Sequence 4, Application US/08705438
/ Patent No. 6015891
/ GENERAL INFORMATION:
/ APPLICANT: Adang, Michael J
/ APPLICANT: Rocheleau, Thomas A.
/ APPLICANT: Merlo, Donald
/ APPLICANT: Murray, Elizabeth E.
/ TITLE OF INVENTION: Synthesis of
/ TITLE OF INVENTION: Gene
/ NUMBER OF SEQUENCES: 9

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 1000 Legion Place, Suite 1750
 CITY: Orlando
 STATE: Florida
 COUNTRY: USA
 ZIP: 32801
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/705,438
 FILING DATE: 29-AUG-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/369,839
 FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88APDA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-705-438-4
 Query Match 92.3%; Score 3144; DB 3; Length 610;
 Best Local Similarity 99.8%; Pred. No. 5,8e-255;
 Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 361 LAVMPSAVYSGVTKEFSDYNDQDEASTQTYDSKRNKAVSWDSIDQLPPTTDEPLEK 420
 QY 468 GYSHOLNTVMCFILOGSRGTIPVLTWTHKSYDFENMIDSKKITOLPIVKAKKLOGSASV 527
 Db 421 GYSHOLNTVMCFILOGSRGTIPVLTWTHKSYDFENMIDSKKITOLPIVKAKKLOGSASV 480
 QY 528 AGPRTGGDIIOCTENGSAATLYTPDVYSQKRYARIHVASTQITFTLSLDGAPFNOY 587
 Db 481 AGPRTGGDIIOCTENGSAATLYTPDVYSQKRYARIHVASTQITFTLSLDGAPFNOY 540
 QY 588 YFDKTIINKGDILTYNSFNLASESTPEELSGNNLOIGVTGLSAGDKVYIDKIEFIPVN 644
 Db 541 YFDKTIINKGDILTYNSFNLASESTPEELSGNNLOIGVTGLSAGDKVYIDKIEFIPVN 597

Search completed: January 10, 2003, 11:08:25
 Job time : 18 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:06:34 ; Search time 11 seconds

(without alignments)
1135.844 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406
Sequence: 1 MNPNNSEHDITKTENNEV.....TGLSAGDKVYIDKIEIFVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	644	10	US-09-943-692-2
2	1214.5	35.7	667	12	US-10-032-717-8
3	1214.5	35.7	673	12	US-10-032-717-18
4	1214.5	35.7	1210	12	US-10-032-717-4
5	1202.5	35.3	673	12	US-10-032-717-12
6	1195.5	35.1	667	12	US-10-032-717-22
7	1194.5	35.1	667	12	US-10-032-717-6
8	1194.5	35.1	669	12	US-10-032-717-10
9	1194.5	35.1	669	12	US-10-032-717-16
10	1194.5	35.1	673	12	US-10-032-717-40
11	1194.5	35.1	1206	12	US-10-032-717-2
12	1192	35.0	670	12	US-10-032-717-44
13	1189	34.9	670	12	US-10-032-717-24
14	1103.5	32.4	620	12	US-10-032-717-32
15	1096.5	32.2	620	12	US-10-032-717-32
16	1095.5	32.2	616	12	US-10-032-717-20
17	1095.5	32.2	620	12	US-10-032-717-42
18	1093	32.1	617	12	US-10-032-717-46
19	1090	32.0	617	12	US-10-032-717-34

20	1063.5	31.2	643	10	US-09-826-660-25	Sequence 25, Appl
21	1063.5	31.2	1166	10	US-09-826-660-23	Sequence 23, Appl
22	1044.5	30.7	655	10	US-09-826-660-27	Sequence 27, Appl
23	1012.5	29.7	1163	10	US-09-756-526A-2	Sequence 2, Appl1
24	980	28.8	1155	10	US-09-756-643-2	Sequence 2, Appl1
25	973	28.6	1177	10	US-09-873-873-26	Sequence 26, Appl
26	971	28.5	1177	10	US-09-873-873-28	Sequence 28, Appl
27	971	28.5	1177	10	US-09-873-873-34	Sequence 34, Appl
28	970	28.5	1177	10	US-09-873-873-10	Sequence 10, Appl
29	970	28.5	1177	10	US-09-873-873-12	Sequence 12, Appl
30	970	28.5	1177	10	US-09-873-873-14	Sequence 14, Appl
31	944.5	27.7	1163	10	US-09-826-660-21	Sequence 21, Appl
32	885	26.0	1193	10	US-09-873-873-30	Sequence 30, Appl
33	883.5	25.9	605	10	US-09-826-660-4	Sequence 4, Appl1
34	883.5	25.9	1148	10	US-09-826-660-2	Sequence 2, Appl1
35	883.5	25.9	1174	10	US-09-826-660-6	Sequence 6, Appl1
36	873.5	25.6	1316	9	US-10-120-544A-4	Sequence 4, Appl1
37	847	24.9	1332	9	US-10-120-544A-18	Sequence 18, Appl
38	845.5	24.8	1156	10	US-09-826-660-15	Sequence 15, Appl
39	845.5	24.8	1178	10	US-09-851-194-2	Sequence 2, Appl1
40	805	23.6	1386	9	US-10-120-544A-6	Sequence 6, Appl1
41	797.5	23.4	1344	9	US-10-120-544A-20	Sequence 20, Appl1
42	627	18.4	1109	10	US-09-756-526A-4	Sequence 4, Appl1
43	538.5	15.8	333	10	US-09-851-194-4	Sequence 4, Appl1
44	399	11.7	265	9	US-10-120-544A-8	Sequence 8, Appl1
45	391	11.5	153	9	US-10-120-544A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-943-692-2
; Sequence 2, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOET:195-1
; CURRENT APPLICATION NUMBER: US/09/943,692
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; PRIOR FILING DATE: 1998-02-23
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 2
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric toxin
US-09-943-692-2

Query Match 100.0%; Score 3406; DB 10; Length 644;
Best local Similarity 100.0%; Pred. No. 3e-258;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNSEHDITKTENNEVPTNHVOYPLAEPNPPTLEDLNTKEFLRMTADNNTLEADSS 60
DB 1 MNPNNSEHDITKTENNEVPTNHVOYPLAEPNPPTLEDLNTKEFLRMTADNNTLEADSS 60
QY 61 TTRDVIOKGISVVDLGGVGFPGALVSFTYNTFNTIMPSEDPKAKMEQVEALMDOK 120
DB 61 TTRDVIOKGISVVDLGGVGFPGALVSFTYNTFNTIMPSEDPKAKMEQVEALMDOK 120
QY 121 IADYAKKALAELOGLQNNVEDVYSLSWOKKPVSSRRPHSGRTRELFSQAESHFRMS 180
DB 121 IADYAKKALAELOGLQNNVEDVYSLSWOKKPVSSRRPHSGRTRELFSQAESHFRMS 180

```

QY 181 MPEFAISGYEVLLTYTAAANTHLFLDKDAQIYGEEMGYEKEDIAEFYKROKLTQOEXT 240
DB 181 MPEFAISGYEVLLTYTAAANTHLFLDKDAQIYGEEMGYEKEDIAEFYKROKLTQOEXT 240
QY 241 DHCVKMYNVLGDLKRGSSYSESWNFRNRRREMTLVLDLALFPLDVLVLYPREVTELT 300
DB 241 DHCVKMYNVLGDLKRGSSYSESWNFRNRRREMTLVLDLALFPLDVLVLYPREVTELT 300
QY 301 RDVLTPIVGVNVLKRGYGTTFNSIENYIRKPHLDYLRHIOFHTRPQPYGNDSPFNYMS 360
DB 301 RDVLTPIVGVNVLKRGYGTTFNSIENYIRKPHLDYLRHIOFHTRPQPYGNDSPFNYMS 360
QY 361 GNVYSTRPISGNDITTSFPGYKSEPEVQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
DB 361 GNVYSTRPISGNDITTSFPGYKSEPEVQNLFEENGKRYRAVANTNLAVMPSAVYSGVT 420
QY 421 KVEFSQYNDQTEBASQYVDSKRNKAVMSDSIDOLPEPTDEPLEKGSQHLNVMCL 480
DB 421 KVEFSQYNDQTEBASQYVDSKRNKAVMSDSIDOLPEPTDEPLEKGSQHLNVMCL 480
QY 481 MGSQRTIVLWTWTHKSYDFNMIDSKITQOLPLVKAAYKLGASGVAVGPRFTGGDIQC 540
DB 481 MGSQRTIVLWTWTHKSYDFNMIDSKITQOLPLVKAAYKLGASGVAVGPRFTGGDIQC 540
QY 541 TENGSAATITVTVDYSQYKRYARHIAVASTQITTLSDGAPENQYTFDKTINKGDTLT 600
DB 541 TENGSAATITVTVDYSQYKRYARHIAVASTQITTLSDGAPENQYTFDKTINKGDTLT 600
QY 601 YNSFNLASFSTPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSTPELSSGNLQIGVGLSAGDKVYIDKIEFIPVN 644

```

RESULT 2

```

US-10-032-717-8
; Sequence 8, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-8

```

```

Query Match 35.7%; Score 1214.5; DB 12; Length 667;
Best Local Similarity 39.0%; Pred. No. 5.3e-87;
Matches 268; Conservative 134; Mismatches 222; Indels 63; Gaps 20;
QY 1 MNPNNRSEHDITKTENNEVPTNVOYPLAETPNPTLEDLNKFEFLMTADNNTALDSS 60
DB 1 MSPNNQNEVEITDPTSTSVSDNSNRYPFANPTNALQNDNDYDYLKMSAGNASEYGPSP 60
QY 61 -----TTROVIOKGISVVDLLGVGFPGALVSFYTNFTLNTWPS--EDPMKAFMPOVE 114
DB 61 EVLVSQDAKAAKALDIYGLSLGVPFVPIVSLYQLDILMPSQKQSMWELPHEQVE 120
QY 115 ALMDOKRADAKKAALELDGLQNNVEDIYSAISSWQKNVSSRNPHSQRIRLEFSQAE 174
DB 115 ALMDOKRADAKKAALELDGLQNNVEDIYSAISSWQKNVSSRNPHSQRIRLEFSQAE 174

```

```

DB 121 ELINOKIAEVARANKALSELEGGNNYQILALAEKKNENPGSR---ALRDVNRNFEILD 177
QY 175 SHFRSMSPFAISGYEVLLTYTAAANTHLFLDKDAQIYGEEMGYEKEDIAEFYKROK 234
DB 175 SHFRSMSPFAISGYEVLLTYTAAANTHLFLDKDAQIYGEEMGYEKEDIAEFYKROK 234
QY 235 LTOEYTDHCVKMYNVLGDLKRGSSYSESWNFRNRRREMTLVLDLALFPLDVLVLYPRE 294
DB 235 LTOEYTDHCVKMYNVLGDLKRGSSYSESWNFRNRRREMTLVLDLALFPLDVLVLYPRE 294
QY 295 VKTELTRDVLTPDPIVGVNVLKRGYGTTFNSIENYIRKPHLDYLRHIOFHTRPQPYG 345
DB 295 VKTELTRDVLTPDPIVGVNVLKRGYGTTFNSIENYIRKPHLDYLRHIOFHTRPQPYG 345
QY 346 FQPGYVYNDSPFNWYSGYVSTRPSISNDITTSFPGYKSEPEVQNLFEENGKRYRAV 404
DB 346 FQPGYVYNDSPFNWYSGYVSTRPSISNDITTSFPGYKSEPEVQNLFEENGKRYRAV 404
QY 405 NTNL---AVMP--SAVYSGVTKVEFSQYNDQTEBASQYVDSKRNKAVMSDSIDOLP 458
DB 405 NTNL---AVMP--SAVYSGVTKVEFSQYNDQTEBASQYVDSKRNKAVMSDSIDOLP 458
QY 459 ETTDEPLEKGSQHLNVMCLMGS--RGITPVLWTWTHKSYDFNMIDSKITQOLPLVKA 517
DB 459 ETTDEPLEKGSQHLNVMCLMGS--RGITPVLWTWTHKSYDFNMIDSKITQOLPLVKA 517
QY 518 YKLGSGA-----SVVAGPRFTGGDIQCENGSAAITVTVDYSQYKRYARHIAVAST 571
DB 518 YKLGSGA-----SVVAGPRFTGGDIQCENGSAAITVTVDYSQYKRYARHIAVAST 571
QY 572 QITFTLSDGAPENQYTFDKTINKGDTLTYSNFMLAS-----FST--PPELSSGNLQ 621
DB 572 QITFTLSDGAPENQYTFDKTINKGDTLTYSNFMLAS-----FST--PPELSSGNLQ 621
QY 622 -----IGVTLGASDKVYIDKIEFIPVN 644
DB 622 -----IGVTLGASDKVYIDKIEFIPVN 644
QY 648 AEDFLGI-----EAYIDRIEIPVD 667
DB 648 AEDFLGI-----EAYIDRIEIPVD 667

```

RESULT 3

```

US-10-032-717-18
; Sequence 18, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-18

```

```

Query Match 35.7%; Score 1214.5; DB 12; Length 673;
Best Local Similarity 39.0%; Pred. No. 5.4e-87;
Matches 268; Conservative 134; Mismatches 222; Indels 63; Gaps 20;
QY 1 MNPNNRSEHDITKTENNEVPTNVOYPLAETPNPTLEDLNKFEFLMTADNNTALDSS 60
DB 1 MSPNNQNEVEITDPTSTSVSDNSNRYPFANPTNALQNDNDYDYLKMSAGNASEYGPSP 60

```



```

Oy 61 ----TTKDVIOKGISVGDLLGVGFPFGALVSEFYTNFLNTMPS--EDPMKAFMEQVE 114
Db 61 EYLVSGDAAKAAADIDYKLLSGVGPVPSLYTQDILIMPSGQKQOMEIFMEQVE 120
Oy 115 ALMDOKIADYAKKALAELOGLONNVEDYVSLSSWQKNPVSRRPHSGGRIRLEFSQAE 174
Db 121 ELINOKIAEYAKKALAELEGLGNNOYLYTALBEMKENPMSR--ALDVRNRFELD 177
Oy 175 SHFRNSMPSFAISGEVLEFYTAQAANTHFLKDAQIYGEEMXEKEDIAEYKROK 234
Db 178 SLFQYMPSEFVATNEVPELVYTOAANHLKLDASIFGEEMGSTTTINNYYDRQK 237
Oy 235 LTOEYTHDCVWYVNGDLKLGSSYESVWNNRNRREMTLVLDLALFPLYDVRLYPKE 294
Db 238 LTAESYSDHCWYETGLAKLGTSKAKOWDYNOFRREMTLVLDVVALFPHYDRTYPM 297
Oy 295 VTELTDRVLTDPYGVNNLRGCT-----TFSNIE-NYIRKPHLDYLRHQFHR-- 345
Db 298 TKAOLTRREYVTDPL-GAVNVSSIGSWYDKAPSGVIESVIRPPHVEDYIGLVYQSR 356
Oy 346 -FQPGYVNDSEFNWSGAVYSTRPSIGSNDITTSPEYGNKSEPYQNLFEKGEYRAVA 404
Db 357 SSSSARY-----IRHAGHQSISYH-RIFSDNIIKQYGTNQHJSTDFETNYDIKTL 411
Oy 405 NTNL---AVMP--SAVYSGVTRKVEFSQYNDQDEASTQYDS-KRNVGAVMSIDOLP 458
Db 412 KDAVLDDIVFPGYTYIFFGMPVEFEFMYNQLNTRKTLKYNVSKDIINGRDSLELEPP 471
Oy 459 ETTDEPLEKGYSHQNLVWYCFMLOGS-RGTIPVLWTHKSVDFENMIDSKITOLPLYKA 517
Db 472 ETSDDQPNYESYHRLCHITSIPATGSTGLVPEFSWTHRSADLIANAHSKTIOLPYKV 531
Oy 518 YKLQSGA-----SYVAGPRTGDIIOCTENGSAATYIVPDVYSQYKRAIRHAYSTS 571
Db 532 SDLAPSLTGPNNTVYSGFGTGGIIRYIRNGVLIISHRKVKSIDINKEYSMRIRYASAN 591
Oy 572 QITFTLSLDCAPNO---YFQDKTINKGDTLYNSFNLAS-----FST--PEELSGNNIQ 621
Db 592 NTEFYIN---PSEENVKSHAQTMNRGALTYNNFNATLPRIKFTTEPTTGAIFE 647
Oy 622 ----IGVTGLSAGDKVYIDKIEFIPVN 644
Db 648 AEDFLGI-----EAYIDRIEFIPVD 667

RESULT 4
US-10-032-717-4
Sequence 4, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flanagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1210
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-032-717-4

Query Match 35.7%; Score 1214.5; DB 12; Length 1210;
Best Local Similarity 39.0%; Pred. No. 1.3e-86;

```

```

Matches 268; Conservative 134; Mismatches 222; Indels 63; Gaps 20;
Oy 1 MNPNNRSEHDTIKTENNENPTNHOYPLAETPPLLEDINTREFLMTADNNTALDSS 60
Db 1 MSPNNQNEIELIDATPSTSVSNDNSNRYPFANEPTNALONNDYDKMSAGNASEYGPSP 60
Oy 61 ----TTKDVIOKGISVGDLLGVGFPFGALVSEFYTNFLNTMPS--EDPMKAFMEQVE 114
Db 61 EYLVSGDAAKAAADIDYKLLSGVGPVPSLYTQDILIMPSGQKQOMEIFMEQVE 120
Oy 115 ALMDOKIADYAKKALAELOGLONNVEDYVSLSSWQKNPVSRRPHSGGRIRLEFSQAE 174
Db 121 ELINOKIAEYAKKALAELEGLGNNOYLYTALBEMKENPMSR--ALDVRNRFELD 177
Oy 175 SHFRNSMPSFAISGEVLEFYTAQAANTHFLKDAQIYGEEMXEKEDIAEYKROK 234
Db 178 SLFQYMPSEFVATNEVPELVYTOAANHLKLDASIFGEEMGSTTTINNYYDRQK 237
Oy 235 LTOEYTHDCVWYVNGDLKLGSSYESVWNNRNRREMTLVLDLALFPLYDVRLYPKE 294
Db 238 LTAESYSDHCWYETGLAKLGTSKAKOWDYNOFRREMTLVLDVVALFPHYDRTYPM 297
Oy 295 VTELTDRVLTDPYGVNNLRGCT-----TFSNIE-NYIRKPHLDYLRHQFHR-- 345
Db 298 TKAOLTRREYVTDPL-GAVNVSSIGSWYDKAPSGVIESVIRPPHVEDYIGLVYQSR 356
Oy 346 -FQPGYVNDSEFNWSGAVYSTRPSIGSNDITTSPEYGNKSEPYQNLFEKGEYRAVA 404
Db 357 SSSSARY-----IRHAGHQSISYH-RIFSDNIIKQYGTNQHJSTDFETNYDIKTL 411
Oy 405 NTNL---AVMP--SAVYSGVTRKVEFSQYNDQDEASTQYDS-KRNVGAVMSIDOLP 458
Db 412 KDAVLDDIVFPGYTYIFFGMPVEFEFMYNQLNTRKTLKYNVSKDIINGRDSLELEPP 471
Oy 459 ETTDEPLEKGYSHQNLVWYCFMLOGS-RGTIPVLWTHKSVDFENMIDSKITOLPLYKA 517
Db 472 ETSDDQPNYESYHRLCHITSIPATGSTGLVPEFSWTHRSADLIANAHSKTIOLPYKV 531
Oy 518 YKLQSGA-----SYVAGPRTGDIIOCTENGSAATYIVPDVYSQYKRAIRHAYSTS 571
Db 532 SDLAPSLTGPNNTVYSGFGTGGIIRYIRNGVLIISHRKVKSIDINKEYSMRIRYASAN 591
Oy 572 QITFTLSLDCAPNO---YFQDKTINKGDTLYNSFNLAS-----FST--PEELSGNNIQ 621
Db 592 NTEFYIN---PSEENVKSHAQTMNRGALTYNNFNATLPRIKFTTEPTTGAIFE 647
Oy 622 ----IGVTGLSAGDKVYIDKIEFIPVN 644
Db 648 AEDFLGI-----EAYIDRIEFIPVD 667

RESULT 5
US-10-032-717-12
Sequence 12, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flanagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 673

```

TYPE: PRT
ORGANISM: *Bacillus thuringiensis* (mutated)
US-10-032-717-12

Query Match 35.3%; Score 1202.5; DB 12; Length 673;
Best Local Similarity 39.1%; Pred. No. 4.7e-86;
Matches 268; Conservative 132; Mismatches 226; Indels 59; Gaps 21;

```

OY 1 MNPNNRSHDTIKTENNVPPTNHVQYPLAETPNPLEDLYNKEFLRMADNTEALDSS 60
DB 1 MSPNNQNEYEIIDATPSTSVSDNSNRYPFANPEPTNALQOMDQKDLKMSAGNASEYPCSP 60
OY 61 ----TKKDIQKISVYVGLLVGVEPPGALVSYFTNFINTIPTS--EDPKAFMEQVE 114
DB 61 EVLVSGODAKAALIDIVKLGSLGVFPVGPVLSYLTQDILIMPSEKQWEIEMEVE 120
OY 115 ALMDQKIADYAKNKAALAELOGLQNNVEDVYALSQKPNPSSRNPHSGR-IRELFSGA 173
DB 121 ELINOKIAEYAKNKAALAELOGLQNNYQYLTLEEMENPNSGRALRDVRRFEIL 180
OY 174 ESHFRNMPSPFALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEKEDIAEYKROL 233
DB 181 DSLFYQYMPSPFALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEETINNYYDRQM 240
OY 234 KLTOEYDHCCKWYNGVLDKLRSSYESWVNFNRRREMTLYLDLALFPLYDVLYPK 293
DB 241 KLTAEYSDHCCKWYNGVLDKLRSSYESWVNFNRRREMTLYLDLALFPLYDVLYPK 300
OY 294 EVKTELTDVLTDPYGVNNLRGYGT-----TFSNIE-NYIRKPHLPDYLRHIOFHR- 345
DB 301 ETKAQLTREVYTDPL-GAVNVSSISGWYDKAPSEGVIESVIRPHVFDYITGLTYTQS 359
OY 346 --FQPGYGNDSFNWYSGNVYS-TRPSIGSNDIITSPPYG-KKSEPVONLEFNGEKYR 401
DB 360 RSISSARY-----IRHWAGHISTYHRSRGSN---LOOMYGTNOMLHSTSTEDFTNYDIYK 412
OY 402 AVANTNL---AVMP--SAVYSGVTKVEFSQYNDQIDEASTQYDS-KRNVGAVMSDSIQ 455
DB 413 TLSKQAVLDIIVPGYTYIFFGMPVEVEFPMVNOINRTKLYNPVSKDIIASTRDELE 472
OY 456 LPPEITDEPLEKYSQOLNYVMCFLMQ--SRGTIPVLTWTHKSVDFFNMIDSKKITQPL 514
DB 473 LPPEITDQPNYESYSHRLCHITISIPATGNTGLVPFWSWTHRSADLNMNTIYSDKITQIPA 532
OY 515 VKAYKLGASVAVAGPRTGDIIOCTEN-GSAATIVYTP--DVSYSOKYARAHVAST 570
DB 533 VKCWDNLPEVPVAKGPGHGTGDLQYNRSTGSVGTFLARGLALEKAGKYRRLRYATD 592
OY 571 SQTFTLSLDGAPFNQYEDKTIKNGDILTYNSFNLSFSTPEELS-----GNN 619
DB 593 ADI--VLHVND--QIOMPKTMNGEDLTSKTFKVADAITLTNLATDSSLALKNLGED 647
OY 620 LOIGVGLSAGDKYIDKIEFIPV 644
DB 648 PNSTLSGI-----YVDRIEFIPVD 667

```

RESULT 6
US-10-032-717-22

Sequence 22, Application US/10032717

Patent No. US20020151709A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Nicholas B. Duck

APPLICANT: Xiang Feng

APPLICANT: Ronald D. Flannagan

APPLICANT: Theodore W. Kahn

APPLICANT: Lyna E. Sims

TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With

TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

FILE REFERENCE: 35718/237005

CURRENT APPLICATION NUMBER: US/10/032,717

CURRENT FILING DATE: 2001-10-23

PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 673
TYPE: PRT
ORGANISM: *Bacillus thuringiensis* (mutated)
US-10-032-717-22

Query Match 35.1%; Score 1195.5; DB 12; Length 673;
Best Local Similarity 38.8%; Pred. No. 1.7e-85;
Matches 266; Conservative 133; Mismatches 227; Indels 59; Gaps 21;

```

OY 1 MNPNNRSHDTIKTENNVPPTNHVQYPLAETPNPLEDLYNKEFLRMADNTEALDSS 60
DB 1 MSPNNQNEYEIIDATPSTSVSDNSNRYPFANPEPTNALQONNDYDKLMSAGNASEYPCSP 60
OY 61 ----TKKDIQKISVYVGLLVGVEPPGALVSYFTNFINTIPTS--EDPKAFMEQVE 114
DB 61 EVLVSGODAKAALIDIVKLGSLGVFPVGPVLSYLTQDILIMPSEKQWEIEMEVE 120
OY 115 ALMDQKIADYAKNKAALAELOGLQNNVEDVYALSQKPNPSSRNPHSGR-IRELFSGA 173
DB 121 ELINOKIAEYAKNKAALAELOGLQNNYQYLTLEEMENPNSGRALRDVRRFEIL 180
OY 174 ESHFRNMPSPFALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEKEDIAEYKROL 233
DB 181 DSLFYQYMPSPFALISGYEVLFTTYAOAANTHLFLKDAQIYGEEMGYEETINNYYDRQM 240
OY 234 KLTOEYDHCCKWYNGVLDKLRSSYESWVNFNRRREMTLYLDLALFPLYDVLYPK 293
DB 241 KLTAEYSDHCCKWYNGVLDKLRSSYESWVNFNRRREMTLYLDLALFPLYDVLYPK 300
OY 294 EVKTELTDVLTDPYGVNNLRGYGT-----TFSNIE-NYIRKPHLPDYLRHIOFHR- 345
DB 301 ETKAQLTREVYTDPL-GAVNVSSISGWYDKAPSEGVIESVIRPHVFDYITGLTYTQS 359
OY 346 --FQPGYGNDSFNWYSGNVYS-TRPSIGSNDIITSPPYG-KKSEPVONLEFNGEKYR 401
DB 360 RSISSARY-----IRHWAGHISTYHRSRGSN---LOOMYGTNOMLHSTSTEDFTNYDIYK 412
OY 402 AVANTNL---AVMP--SAVYSGVTKVEFSQYNDQIDEASTQYDS-KRNVGAVMSDSIQ 455
DB 413 TLSKQAVLDIIVPGYTYIFFGMPVEVEFPMVNOINRTKLYNPVSKDIIASTRDELE 472
OY 456 LPPEITDEPLEKYSQOLNYVMCFLMQ--SRGTIPVLTWTHKSVDFFNMIDSKKITQPL 514
DB 473 LPPEITDQPNYESYSHRLCHITISIPATGNTGLVPFWSWTHRSADLNMNTIYSDKITQIPA 532
OY 515 VKAYKLGASVAVAGPRTGDIIOCTEN-GSAATIVYTP--DVSYSOKYARAHVAST 570
DB 533 VKCWDNLPEVPVAKGPGHGTGDLQYNRSTGSVGTFLARGLALEKAGKYRRLRYATD 592
OY 571 SQTFTLSLDGAPFNQYEDKTIKNGDILTYNSFNLSFSTPEELS-----GNN 619
DB 593 ADI--VLHVND--QIOMPKTMNGEDLTSKTFKVADAITLTNLATDSSLALKNLGED 647
OY 620 LOIGVGLSAGDKYIDKIEFIPV 644
DB 648 PNSTLSGI-----YVDRIEFIPVD 667

```

RESULT 7
US-10-032-717-6

Sequence 6, Application US/10032717

Patent No. US20020151709A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Nicholas B. Duck

APPLICANT: Xiang Feng

APPLICANT: Ronald D. Flannagan

APPLICANT: Theodore W. Kahn

APPLICANT: Lynn E. Slims
 TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
 FILE REFERENCE: 35718/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 PRIOR FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 667
 TYPE: PRT
 ORGANISM: Bacillus thuringiensis (truncated)
 US-10-032-717-6

Query Match 35.1%; Score 1194.5; DB 12; Length 667;
 Best Local Similarity 38.9%; Pred. No. 2e-85;
 Matches 266; Conservative 133; Mismatches 224; Indels 61; Gaps 21;

1 MNPNNSEHDITKTENNENPTNHYQPLAETPNPTLEDLNTKEPLMTADNTEALDSS 60
 1 MSPNNONEEIIDATPSTVSNDNSNRYPANPEPTNALQNDYKDLKMSAGNASEVPGSP 60
 61 ----TKDYIQGISVGDLLGVGFPFGALVSTYTNFLNTIWS--EDPKAFMEQVE 114
 61 EVLVSGODAKAKAIDIVGKILSGIVPFGPIVSLYTOLIDILMPGSEKQWEIEMEVE 120
 115 ALMDOKIADYARKKALAELOGLONNVEDYVSAISSKOKNPVSSRNPHSGRIEELSQA 174
 121 ELINOKIAEYARKKALAELOGLONNVEDYVSAISSKOKNPVSSRNPHSGRIEELSQA 177
 175 SFRNNSMPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEWYKEDIAEYKROK 234
 178 SFTQYMPSEFVYVNFEPFLTYAQAANTHLFLKDAQIYGEWYKEDIAEYKROK 237
 235 LTOEDYDHCYKWTNVLGDLKRGSSYSEWYFNRRRMTLYDIALPFLYVRLPYKE 294
 238 LTAEYSDHCYKWTNVLGDLKRGSSYSEWYFNRRRMTLYDIALPFLYVRLPYKE 297
 295 VKTELTRDYLDPIVGNLRLGYGT-----TFSNIE-NYIRKPHLDYLRIOFHTR-- 345
 298 TKAOITREYTDPL-GAVNVSSISGWDKAPSGVIESSVIRPHVFDYITGLVYTOGR 356
 346 -POPGYGNDSFNWYSGNYS--TRPSIGSNDITTSFPG--NKSEPVOLNEFNGEYKRA 402
 357 SISARY-----IRHWAGHOISYHRVSRGSN---LOQMYGTNOMLHSTFEDFTNYDIYKT 409
 403 VANTNL---AVWP--SAVYSGVTKVEFSOYNDOTDEASTQYDS--KRVGAVSMDSIDOL 456
 410 LSKDAVLDIVYGYTYIFFGMPEVEEFVWVNOQNLNTRKTLKYNVSQDIIASTRDSLEL 469
 457 PPTTDEPLEKGYSHOLNVCFLMOG--SRGTIPVLWTNTHKSVDFENMIDSKRIITQLPLV 515
 470 PPTSDQPNYESYSHRCHITISIPATGNTTGLVPSVWTHRSADLNTIYSDITQIPAV 529
 516 KAYKLGASGVAVAPRPTGDDIIOCTEN-GSAATITVTP--DVSYSOKYRAIRHYASTS 571
 530 KCMONLPEFVYVVGPGTGLDLOYNRSTGVSGLFLARGLALEKAGRYRVLRYATDA 589
 572 QITPFLSIDGAPFNOYFEDTKINKGDTLYNSFNLASSTPEELS-----GNL 620
 590 DI--VLHVND---QIOMPRTMNGEDLTKTEKVAADAITTLNLATDSSIALKHNIGEDP 644
 621 QIGVYGLSAGDKVYIDKIEFIPIVN 644
 645 NSTLSGI-----YYVDRIEFIPVD 663

RESULT 8
 US-10-032-717-10
 : Sequence 10, Application US/10032717
 : Patent No. US20020151709A1

GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Nicholas B. Duck
 APPLICANT: Xiang Feng
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Theodore W. Kahn
 APPLICANT: Lynn E. Slims
 TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
 FILE REFERENCE: 35718/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 PRIOR FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 10
 LENGTH: 669
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Maize optimized cry1218-1
 US-10-032-717-10

Query Match 35.1%; Score 1194.5; DB 12; Length 669;
 Best Local Similarity 38.9%; Pred. No. 2e-85;
 Matches 266; Conservative 133; Mismatches 224; Indels 61; Gaps 21;

1 MNPNNSEHDITKTENNENPTNHYQPLAETPNPTLEDLNTKEPLMTADNTEALDSS 60
 1 MSPNNONEEIIDATPSTVSNDNSNRYPANPEPTNALQNDYKDLKMSAGNASEVPGSP 60
 61 ----TKDYIQGISVGDLLGVGFPFGALVSTYTNFLNTIWS--EDPKAFMEQVE 114
 61 EVLVSGODAKAKAIDIVGKILSGIVPFGPIVSLYTOLIDILMPGSEKQWEIEMEVE 120
 115 ALMDOKIADYARKKALAELOGLONNVEDYVSAISSKOKNPVSSRNPHSGRIEELSQA 174
 121 ELINOKIAEYARKKALAELOGLONNVEDYVSAISSKOKNPVSSRNPHSGRIEELSQA 177
 175 SFRNNSMPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEWYKEDIAEYKROK 234
 178 SFTQYMPSEFVYVNFEPFLTYAQAANTHLFLKDAQIYGEWYKEDIAEYKROK 237
 235 LTOEDYDHCYKWTNVLGDLKRGSSYSEWYFNRRRMTLYDIALPFLYVRLPYKE 294
 238 LTAEYSDHCYKWTNVLGDLKRGSSYSEWYFNRRRMTLYDIALPFLYVRLPYKE 297
 295 VKTELTRDYLDPIVGNLRLGYGT-----TFSNIE-NYIRKPHLDYLRIOFHTR-- 345
 298 TKAOITREYTDPL-GAVNVSSISGWDKAPSGVIESSVIRPHVFDYITGLVYTOGR 356
 346 -POPGYGNDSFNWYSGNYS--TRPSIGSNDITTSFPG--NKSEPVOLNEFNGEYKRA 402
 357 SISARY-----IRHWAGHOISYHRVSRGSN---LOQMYGTNOMLHSTFEDFTNYDIYKT 409
 403 VANTNL---AVWP--SAVYSGVTKVEFSOYNDOTDEASTQYDS--KRVGAVSMDSIDOL 456
 410 LSKDAVLDIVYGYTYIFFGMPEVEEFVWVNOQNLNTRKTLKYNVSQDIIASTRDSLEL 469
 457 PPTTDEPLEKGYSHOLNVCFLMOG--SRGTIPVLWTNTHKSVDFENMIDSKRIITQLPLV 515
 470 PPTSDQPNYESYSHRCHITISIPATGNTTGLVPSVWTHRSADLNTIYSDITQIPAV 529
 516 KAYKLGASGVAVAPRPTGDDIIOCTEN-GSAATITVTP--DVSYSOKYRAIRHYASTS 571
 530 KCMONLPEFVYVVGPGTGLDLOYNRSTGVSGLFLARGLALEKAGRYRVLRYATDA 589
 572 QITPFLSIDGAPFNOYFEDTKINKGDTLYNSFNLASSTPEELS-----GNL 620
 590 DI--VLHVND---QIOMPRTMNGEDLTKTEKVAADAITTLNLATDSSIALKHNIGEDP 644
 621 QIGVYGLSAGDKVYIDKIEFIPIVN 644

Db 645 NSTLSGI-----YVDRIEFIPVD 663

RESULT 9

US-10-032-717-16

Sequence 16, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Slms
TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
PRIORITY FILING DATE: 2001-10-23
PRIORITY FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 669
TYPE: PRT
ORGANISM: *Bacillus thuringiensis* (truncated)
US-10-032-717-16

Query Match 35.1%; Score 1194.5; DB 12; Length 669;
Best Local Similarity 38.9%; Pred. No. 2e-65;
Matches 266; Conservative 133; Mismatches 224; Indels 61; Gaps 21;

QY 1 MNPNNRSEHDITKTENNEVPNHYOPLAETPNPLEDLYNKEFLRMTADNTEALDSS 60
DB 1 MSPNNONEYEIIDATPSTSVSNDNRYPFANEPTNALQNMOKYKOLKMSAGNASEPSP 60
QY 61 -----TTKVOYKIGISVGDGLGVGFPFGALVSFTYNTFLTTPS--EDPMKAMEQVE 114
DB 61 EYLVSGDAKAAIDIVKLLSGLVGVPVGLVSLYTLIDILMPGSEKSGMEIFMEQVE 120
QY 115 ALMDQKIDYAKKALAELOGIANNVEDYVSALSMOKNPVSSRNPHSGRIREFSQA 174
DB 121 ELINOKIAEYARRKALSELEGNNYQVLYLLEEMENPMSGR--ALRDVNRFEILD 177
QY 175 SHFRSMPSFALSGLVFLTYTAQANTHLFLKDAQIYGEWYKEDIKEDIAEYKROK 234
DB 178 SLFTQYMSPFRTNFEVPLTYMAAANLHLKLDASIFGEWGSTTTNNYDQMK 237
QY 235 LTOEYTHDCVMKYNVGLDKLRSSYESVWNNRKRRENTLVLDLALFPLYDYRLPK 294
DB 238 LTAESYSDHCVMKYNVGLDKLRSSYESVWNNRKRRENTLVLDLALFPLYDYRLPK 294
QY 295 VKTELTRDYLDPDLYGVNNGKGYG-----TFSNIE-NYIRKPHLDYLRIOFHT 345
DB 298 TKADLTREVYDPL-GAVNVSSIGSMYDKAPSFVIESVIRPHVDYITGLVYVQSR 356
QY 346 -FOGYYGNDSEFNWSSGYVS-TRPSIGSNDITSPFYG-NKSEPVQONLEFNGEKYRA 402
DB 357 SISSARY-----IRHWAGHQSISYHVSRSN--LQOMYGTQONLHSTFDFTYDIKT 409
QY 403 VANTNL--AWP--SAVYGVTKVEFSQVNDQDEASTQYDS-KNNGAVSNDSDIDOL 456
DB 410 LSKRAVLIDLYPGTYIFFGMPVEFEFMMQNLNNTKTKLYNVSVSDIASTDSELEL 469
QY 457 PPEPTDEPLEKGYSHQNLVYVCLMUG-SRGTPLVLTWTHKSVDFNMIDSKRTQPLV 515
DB 470 PPEPTDQPNESYSHRLCHITSIPATGNTGLVVFESWTHRSADLNTIYSKTIQIPAY 529
QY 516 KAYVLOGSASVAGPRTGGDIIOCTEN-GSAATIVTP--DVYSQKRYARIHASTS 571
DB 530 KCMONLFPVYVAGPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDA 589

QY 572 QITFTLSLDGAPFPNOYEDKTIKNGDILTNSFNLSFSTPEELS-----GNUL 620
DB 590 DI--VLHVND-----QIQMPKTMNGEDLTSKTFKVAADATTLNLATDSLAKNINLEDP 644
QY 621 QIGVYGLSAGDKVYTDKIEFIPV 644
DB 645 NSTLSGI-----YVDRIEFIPVD 663

RESULT 10

US-10-032-717-40

Sequence 40, Application US/10032717
Patent No. US20020151709A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Xiang Feng
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Slms
TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
PRIORITY FILING DATE: 2001-10-23
PRIORITY FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 673
TYPE: PRT
ORGANISM: *Bacillus thuringiensis* (mutated)
US-10-032-717-40

Query Match 35.1%; Score 1194.5; DB 12; Length 673;
Best Local Similarity 38.8%; Pred. No. 2e-65;
Matches 266; Conservative 133; Mismatches 227; Indels 59; Gaps 21;

QY 1 MNPNNRSEHDITKTENNEVPNHYOPLAETPNPLEDLYNKEFLRMTADNTEALDSS 60
DB 1 MSPNNONEYEIIDATPSTSVSNDNRYPFANEPTNALQNMOKYKOLKMSAGNASEPSP 60
QY 61 -----TTKVOYKIGISVGDGLGVGFPFGALVSFTYNTFLTTPS--EDPMKAMEQVE 114
DB 61 EYLVSGDAKAAIDIVKLLSGLVGVPVGLVSLYTLIDILMPGSEKSGMEIFMEQVE 120
QY 115 ALMDQKIDYAKKALAELOGIANNVEDYVSALSMOKNPVSSRNPHSGRIREFSQA 173
DB 121 ELINOKIAEYARRKALSELEGNNYQVLYLLEEMENPMSGR--ALRDVNRFEILD 180
QY 174 SHFRSMPSFALSGLVFLTYTAQANTHLFLKDAQIYGEWYKEDIKEDIAEYKROK 233
DB 181 DSEFTQYMSPFRTNFEVPLTYMAAANLHLKLDASIFGEWGSTTTNNYDQMK 240
QY 234 KLTQYTHDCVMKYNVGLDKLRSSYESVWNNRKRRENTLVLDLALFPLYDYRLPK 293
DB 241 LTAESYSDHCVMKYNVGLDKLRSSYESVWNNRKRRENTLVLDLALFPLYDYRLPK 300
QY 294 EVTTELTRDYLDPDLYGVNNGKGYG-----TFSNIE-NYIRKPHLDYLRIOFHT 345
DB 301 TKADLTREVYDPL-GAVNVSSIGSMYDKAPSFVIESVIRPHVDYITGLVYVQSR 359
QY 346 -FOGYYGNDSEFNWSSGYVS-TRPSIGSNDITSPFYG-NKSEPVQONLEFNGEKYRA 401
DB 360 RSISSARY-----IRHWAGHQSISYHVSRSN--LQOMYGTQONLHSTFDFTYDIKT 412
QY 402 VANTNL--AWP--SAVYGVTKVEFSQVNDQDEASTQYDS-KNNGAVSNDSDIDOL 455
DB 413 LSKRAVLIDLYPGTYIFFGMPVEFEFMMQNLNNTKTKLYNVSVSDIASTDSELEL 472
QY 456 LPEPTDEPLEKGYSHQNLVYVCLMUG-SRGTPLVLTWTHKSVDFNMIDSKRTQPL 514

```

Db 473 LPRETSDOENVESYSHRLCHTISIPATGNTGLVPEFSWTHRSADLNNTIYSDKTIQIPA 532
Qy 515 VYAKYKQASAVYAGPRFGCDIIQCTEN-GSAATITVP---DVSQKYARARIHVAST 570
Db 533 VCKMDLPEVPYVKGHGGHGLDLYNRSTGSGVGLFLARYGLALEKAGKYVRLRYATDA 592
Qy 571 SOTTFTLSLDGAPENQYFDKTIINKGDTLTYSNFNLASFTEPELS-----GNN 619
Db 593 ADI--VLHVADA---QIQMPKTNPCEDILSKTFKVAADITTLNLATDSLAKHNLGSD 647
Qy 620 LQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 648 PNSTLSGI-----VYVDRIEFIPVD 667

RESULT 11
US-10-032-717-2
; Sequence 2, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-032-717-2

Query Match 35.1%; Score 1194.5; DB 12; Length 1206;
Best Local Similarity 38.9%; Pred. No. 4.7e-85;
Matches 266; Conservative 133; Mismatches 224; Indels 61; Gaps 21;

Qy 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPLEDLNKEFLMTADNTEALDSS 60
Db 1 MSPNNQNEYELIIDATPSTSVSNDNRYPFANEPTNALQNDYKDYLMKSGNASEYFGSP 60
Qy 61 ----TTKDVIOKGISVVGDLGVGPPGALVSFTNPLNTIWPSS--EDPWKAFMEQVE 114
Db 61 EVLVSGDAAKAAIDYIGKLLSGIGVPEGPVIVSLYTLQDLILMPGSKSQWEIFMEQVE 120
Qy 115 ALMDOKIADYAKNALAELOGLONNVEDYVSALSSWQKNPVSRRPHSOGRIREFSOAE 174
Db 121 ELINOKIAEYARNAKALSELGELGNNGYOLYLTALEWEMENPNGSR--ALRDVNRREFILD 177
Qy 175 SHFRNSMPSFALISGEVEFLTTYAOAANTHLFLKDAQIYEEWGYEKEDIAEYFROK 234
Db 178 SLFTQYMSERVTNEFEVFLTYVMAANLHLILLKDAISIEEEMGWSTTTINNYDRMK 237
Qy 235 LTOEYTDHCVMYVNGDLKRGSSYESVWVNFRRREMTLVLDLALFPLYDVRLYPE 294
Db 238 LTAESYSDHCVMYETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVALFPYDRTYPM 297
Qy 295 VKTELTRDVLDPITGVANNLKGYGT-----TESNIE-NYIRKPHLFDYLRIQFHTR-- 345
Db 298 TKAQJLTREVYDPL-GAANVSSISGMYKADSEFVIESVLRPPHVEDYITGLVYVTSR 356
Qy 346 -FQPGYGNDSFNWYSGNVYS--TRPSIGSNDITITSPFG-KNSSEPVONLENGEKYRA 402
Db 357 SISSARY-----IRHWAGHDIHYHVRSGSN---LQOMGTGNQNLHSTSTPFDNTDIYKT 409

```

```

Qy 403 VANTNL---AWP--SAVYSGVTVESQVNDQDEASTQTYDS-KRNVGAVSMDSIDOL 456
Db 410 LSKDAVLVDIYVPGYTYIFGMPMEVEEFMNQNLNTRRTKLYNVSVSKDIIASTDSELEL 469
Qy 457 PPRETDEBLEKGYSHQNLVWYCMFLMOG--SRGTIVLMTHTHSVDFPNMIDSKITQOLPV 515
Db 470 PPRETSDOENVESYSHRLCHTISIPATGNTGLVPEFSWTHRSADLNNTIYSDKTIQIPA 529
Qy 516 KAYKIQASAVYAGPRFGCDIIQCTEN-GSAATITVP---DVSQKYARARIHVASTS 571
Db 530 KCMMDLPEVPYVKGHGGHGLDLYNRSTGSGVGLFLARYGLALEKAGKYVRLRYATDA 589
Qy 572 QITFTLSLDGAPENQYFDKTIINKGDTLTYSNFNLASFTEPELS-----GNNL 620
Db 590 DI--VLHVADA---QIQMPKTNPCEDILSKTFKVAADITTLNLATDSLAKHNLGSDP 644
Qy 621 QIGVTGLSAGDKVYIDKIEFIPVN 644
Db 645 NSTLSGI-----VYVDRIEFIPVD 663

```

```

RESULT 12
US-10-032-717-44
; Sequence 44, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-44

```

```

Query Match 35.0%; Score 1192; DB 12; Length 670;
Best Local Similarity 38.7%; Pred. No. 3.1e-85;
Matches 265; Conservative 134; Mismatches 225; Indels 60; Gaps 21;

Qy 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPLEDLNKEFLMTADNTEALDSS 60
Db 1 MSPNNQNEYELIIDATPSTSVSNDNRYPFANEPTNALQNDYKDYLMKSGNASEYFGSP 60
Qy 61 ----TTKDVIOKGISVVGDLGVGPPGALVSFTNPLNTIWPSS--EDPWKAFMEQVE 114
Db 61 EVLVSGDAAKAAIDYIGKLLSGIGVPEGPVIVSLYTLQDLILMPGSKSQWEIFMEQVE 120
Qy 115 ALMDOKIADYAKNALAELOGLONNVEDYVSALSSWQKNPVSRRPHSOGRIREFSOAE 174
Db 121 ELINOKIAEYARNAKALSELGELGNNGYOLYLTALEWEMENL--RMSRALDVNRREFILD 178
Qy 175 SHFRNSMPSFALISGEVEFLTTYAOAANTHLFLKDAQIYEEWGYEKEDIAEYFROK 234
Db 179 SLFTQYMSERVTNEFEVFLTYVMAANLHLILLKDAISIEEEMGWSTTTINNYDRMK 238
Qy 235 LTOEYTDHCVMYVNGDLKRGSSYESVWVNFRRREMTLVLDLALFPLYDVRLYPE 294
Db 239 LTAESYSDHCVMYETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVALFPYDRTYPM 298
Qy 295 VKTELTRDVLDPITGVANNLKGYGT-----TESNIE-NYIRKPHLFDYLRIQFHTR-- 345

```

```

Db 299 TKAOITREYTDPL-GAVNVSSIGSWYDKAPSEGVIESVIRPPEHYDTGLVYTOQR 357
QY 346 -FOGQYNDSEFNWNGNYS--TRPSIGSNDITSPFYG--NKSEPVONLEFNGEYRA 402
Db 358 SISARV-----IRHWAGHOISYHRVRSN---LOOMGTQONLHSTSPFEDNYDITKT 410
QY 403 VANTNL---AVWP--SAVSGVTKVEFQYDQDEASTOTYDS--KRNAGVSWDSIDOL 456
Db 411 LSKDAVLIDIVPGYTYFFGMEPEFVFNQONNTRKTLKYPVSKDIIASTRDELEL 470
QY 457 PPTTDEPLEKGYSHOLNYMCLMOG--SRGTIPVLTWTHKSVDPFNMIDSKRTIOLPLV 515
Db 471 PPTSDQPNYESYSHRCHITTSIPATGNTGLVPEFVSWTHRSADLNNITYSKTIQIPAV 530
QY 516 KAYKIQSGASVYAGPRTGDIIOCTEN--GSAATITVTP---DVSYSQYRARIHYASTS 571
Db 531 KQWMDLPEVYVKGCGHTGDLQYNRSVGTFLARYGLALEKAGKRYRLRYATDA 590
QY 572 QITFTLSLDGAPFNOYFDKTIKNGDITLYNSFNULASFSTPELS-----GNL 620
Db 591 DI--VLHVND---QIQMPKTMNGEDLTSKTEKVAITTLNLATDSLALKHNLGEP 645
QY 621 QICVTGLSAGDKVYIDKIEFIPV 644
Db 646 NSTLSGI-----YVDRIEFIPVD 664

```

RESULT 13

```

US-10-032-717-24
: Sequence 24, Application US/10032717
: Patent No. US20020151709A1
: GENERAL INFORMATION:
: APPLICANT: Andre R. Abad
: APPLICANT: Nicholas B. Duck
: APPLICANT: Xiang Feng
: APPLICANT: Ronald D. Flanagan
: APPLICANT: Theodore W. Kahn
: APPLICANT: Lynn E. Sims
: TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
: TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
: FILE REFERENCE: 35718/237005
: CURRENT APPLICATION NUMBER: US/10/032,717
: PRIOR FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 670
: TYPE: PRT
: ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-24

```

```

Query Match 34.9%; Score 1189; DB 12; Length 670;
Best Local Similarity 38.6%; Pred. No. 5,3e-85;
Matches 264; Conservative 135; Mismatches 225; Indels 60; Gaps 21;

```

```

QY 1 MNPNNRSHDIKITTENNEVPNNOYPLAETPMTLEDLNYKEFLRMTADNTEALDSS 60
Db 1 MSPNNQNEYELIDATPSYVSNDNRYPFANEPTNALQNMIDYKYLKMSAGNASEYGPSP 60
QY 61 -----TTKVIGKISVYGDILGVGPGGALVSFTYNFLNTIPTS--EDPWKAFMCOVE 114
Db 61 EVLVSGDAAKAIDIVGKLSGLVGPVPGIVSLYQILDIMPSEKQWELFMCOVE 120
QY 115 ALMDOKIADYAKKALAELOGIQQNNVEDYVSAISSMOKNPVSSRNPSQGRIRLEFSQAE 174
Db 121 ELINQIAEYARKKALSELGLGNNOYLITALEMEENEL--KMSALADVNRREFILD 178
QY 175 SHFNKSPFSAISGYEVLFTTYAQANLTHFLIKDAQIYGEWGYEKEDIAEYKROK 234
Db 179 SLFOYMSFSAVTFNFEVPLTVYMAANLHLILKLDASIGEEWGMSTTTINNYDROK 238

```

```

QY 235 LFOETDHCYKYNGLDKRGSSYESVNNRREMTLVLIDALEPLDYRLYPE 294
Db 239 LIAEYSDHCYKYNGLDKRGSSYESVNNRREMTLVLIDALEPLDYRLYPE 298
QY 295 VTELTADYLDPIYGVNNLRGCT-----TESNIE--NYIRKPLPYLRIOFHR-- 345
Db 299 TKAOITREYTDPL-GAVNVSSIGSWYDKAPSEGVIESVIRPPEHYDTGLVYTOQR 357
QY 346 -FOGQYNDSEFNWNGNYS--TRPSIGSNDITSPFYG--NKSEPVONLEFNGEYRA 402
Db 358 SISARV-----IRHWAGHOISYHRVRSN---LOOMGTQONLHSTSPFEDNYDITKT 410
QY 403 VANTNL---AVWP--SAVSGVTKVEFQYDQDEASTOTYDS--KRNAGVSWDSIDOL 456
Db 411 LSKDAVLIDIVPGYTYFFGMEPEFVFNQONNTRKTLKYPVSKDIIASTRDELEL 470
QY 457 PPTTDEPLEKGYSHOLNYMCLMOG--SRGTIPVLTWTHKSVDPFNMIDSKRTIOLPLV 515
Db 471 PPTSDQPNYESYSHRCHITTSIPATGNTGLVPEFVSWTHRSADLNNITYSKTIQIPAV 530
QY 516 KAYKIQSGASVYAGPRTGDIIOCTEN--GSAATITVTP---DVSYSQYRARIHYASTS 571
Db 531 KQWMDLPEVYVKGCGHTGDLQYNRSVGTFLARYGLALEKAGKRYRLRYATDA 590
QY 572 QITFTLSLDGAPFNOYFDKTIKNGDITLYNSFNULASFSTPELS-----GNL 620
Db 591 DI--VLHVND---QIQMPKTMNGEDLTSKTEKVAITTLNLATDSLALKHNLGEP 645
QY 621 QICVTGLSAGDKVYIDKIEFIPV 644
Db 646 NSTLSGI-----YVDRIEFIPVD 664

```

RESULT 14

```

US-10-032-717-30
: Sequence 30, Application US/10032717
: Patent No. US20020151709A1
: GENERAL INFORMATION:
: APPLICANT: Andre R. Abad
: APPLICANT: Nicholas B. Duck
: APPLICANT: Xiang Feng
: APPLICANT: Ronald D. Flanagan
: APPLICANT: Theodore W. Kahn
: APPLICANT: Lynn E. Sims
: TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
: TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
: FILE REFERENCE: 35718/237005
: CURRENT APPLICATION NUMBER: US/10/032,717
: PRIOR FILING DATE: 2001-10-23
: PRIOR APPLICATION NUMBER: 60/242,838
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 620
: TYPE: PRT
: ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-30

```

```

Query Match 32.4%; Score 1103.5; DB 12; Length 620;
Best Local Similarity 39.5%; Pred. No. 2.3e-78;
Matches 252; Conservative 117; Mismatches 210; Indels 59; Gaps 21;

```

```

QY 48 MTADNTEALDSS-----TKDYIQRKISVYGDILGVGPGGALVSFTYNFLNTIPTS- 102
Db 1 MSAGNASEYGPSPVSVSGDAAKAIDIVGKLSGLVGPVPGIVSLYQILDIMPSPG 60
QY 103 -EDPWKAFMCOVEALMDOKIADYAKKALAELOGIQQNNVEDYVSAISSMOKNPVSSRNPH 161
Db 61 EKSQWELFMCOVEELINQIAEYARKKALSELGLGNNOYLITALEMEENPNRSGS 120
QY 162 SQGR-IRLEFSQAEHFNMSPSAISGYEVLFTTYAQANLTHFLIKDAQIYGEWGY 220

```

```

Db 121 RALDVNNREELIDSLTQYMPSEFRVNFEPPLTYVAMANLHLKLSKASJEGEEMGW 180
QY 221 EKEDIAEFYKROLKLTQETDHCVKMYNVLGDLKRGSSYESVWVNFNRRREMTLVLDLI 280
Db 181 STTTINNYDROKMLTAEDSDHCWKWYETGLAKTSAKQWVDYNOFRREMTLAVLDVY 240
QY 281 ALFPLVDVLYKREVKETELTRVDLPDPIYGVNMLRGYGT-----TFSNIE-NYIRKPHL 333
Db 241 ALFPNDTIRTYPMETKAQLTRREYTDPL-GAVNVSSIGSWYDKAPSGVIESSVIRPPHV 299
QY 334 EDVLRHQFTR---FQPGYGNDSFNWMSGNYVS-TRPSIGSNDITTSFYG-NKSSP 388
Db 300 FDIITGLTYTQSRSSSAR-----IRHMGHQSITHRSRGSN---LQOMTGTNQLHS 352
QY 389 VONLEFNGEKYRAVANLNL---AWP--SAVYSGVTKVEFSQYNDQDEASTQYDS-K 442
Db 353 TSFDFNTNDIYKTLSDAVLDIYVPGYTYIFGMPVEFEFVNVQNLNTRKTLKYNPVS 412
QY 443 RNVGAVMSDIDLPETDEPLEKGYSHQNLVWCFMOC-SRGTIVLYLWTHKSVDF 501
Db 413 KDIASRDELELPETSDQPNYESYSHRLCHITSIPATGNTGLVPVFSWTHRSADLN 472
QY 502 NMIDSKITQLPLVYAKKLOGSASVYAGPRFTGDIIOCTEN-GSAATIVYTP---DVS 557
Db 473 NTIYSDKITQIPAVKCMQDLPEVPVYKGGHGTGDLQYNRSTGSGVGLFLARYGLALEK 532
QY 558 SOKYRARIHYASTQITFTLSLDGAPFNOYFDKTIKNGDITLYNSFNILASFSTPELS- 616
Db 533 AGKYRVRIRYATDADI--VLHVND--QIOMPKTMNPGEDLTSKTFKVAADATITLNLAT 587
QY 617 -----GNNLOIGVYGLSAGDKYIYDKIEFIPVN 644
Db 588 DSSLALKNLGEDPNSTLSGI-----VYVDRIEFIPVD 620

```

RESULT 15 US-10-032-717-32

```

; Sequence 32, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1e1 Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
; US-10-032-717-32

```

Query Match 32.2%; Score 1096.5; DB 12; Length 620;
Best Local Similarity 39.2%; Pred. No. 7.9e-78;
Matches 250; Conservative 118; Mismatches 211; Indels 59; Gaps 21;

```

QY 48 MPADNTEALDSS---TTKDVIOKGISVVDLGVGPFPGALVSFTYNFLNTMP- 102
Db 1 MSAGNSSEYGPSPVLSQDAKAAIDIVGKLSGLGVFPVGPVYSITLTOLDIIMP 60
QY 103 -EDPMKAFMEQVADMDOKIADYAKKALAELOGLONNVEDVYSAISSWQKNFVSSRNPH 161
Db 61 EKQWEIFMEQVDELINOKIAEYARNKALSELGLGNNYQVLYLTALKEWENPLKMSNGS 120

```

```

QY 162 SOGR-IRELESOAESHRFNSMPSFASISGVEVLELTYYAOANTHLELKDAQIYGEEMGY 220
Db 121 RALDVNNREELIDSLTQYMPSEFRVNFEPPLTYVAMANLHLKLSKASJEGEEMGW 180
QY 221 EKEDIAEFYKROLKLTQETDHCVKMYNVLGDLKRGSSYESVWVNFNRRREMTLVLDLI 280
Db 181 STTTINNYDROKMLTAEDSDHCWKWYETGLAKTSAKQWVDYNOFRREMTLAVLDVY 240
QY 281 ALFPLVDVLYKREVKETELTRVDLPDPIYGVNMLRGYGT-----TFSNIE-NYIRKPHL 333
Db 241 ALFPNDTIRTYPMETKAQLTRREYTDPL-GAVNVSSIGSWYDKAPSGVIESSVIRPPHV 299
QY 334 EDVLRHQFTR---FQPGYGNDSFNWMSGNYVS-TRPSIGSNDITTSFYG-NKSSP 388
Db 300 FDIITGLTYTQSRSSSAR-----IRHMGHQSITHRSRGSN---LQOMTGTNQLHS 352
QY 389 VONLEFNGEKYRAVANLNL---AWP--SAVYSGVTKVEFSQYNDQDEASTQYDS-K 442
Db 353 TSFDFNTNDIYKTLSDAVLDIYVPGYTYIFGMPVEFEFVNVQNLNTRKTLKYNPVS 412
QY 443 RNVGAVMSDIDLPETDEPLEKGYSHQNLVWCFMOC-SRGTIVLYLWTHKSVDF 501
Db 413 KDIASRDELELPETSDQPNYESYSHRLCHITSIPATGNTGLVPVFSWTHRSADLN 472
QY 502 NMIDSKITQLPLVYAKKLOGSASVYAGPRFTGDIIOCTEN-GSAATIVYTP---DVS 557
Db 473 NTIYSDKITQIPAVKCMQDLPEVPVYKGGHGTGDLQYNRSTGSGVGLFLARYGLALEK 532
QY 558 SOKYRARIHYASTQITFTLSLDGAPFNOYFDKTIKNGDITLYNSFNILASFSTPELS- 616
Db 533 AGKYRVRIRYATDADI--VLHVND--QIOMPKTMNPGEDLTSKTFKVAADATITLNLAT 587
QY 617 -----GNNLOIGVYGLSAGDKYIYDKIEFIPVN 644
Db 588 DSSLALKNLGEDPNSTLSGI-----VYVDRIEFIPVD 620

```

Search completed: January 10, 2003, 11:08:43
Job time : 13 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:04:59 ; Search time 21 Seconds
(without alignments)

2948.122 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406

Sequence: 1 MHPNNRSEHDTIKTENNEV.....TGLSAGDKVYIDKIEFIPVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3406	100.0	652	2 A27323	parasporal crystal
2	2564.5	75.3	649	1 JH0261	parasporal crystal
3	2341.5	68.7	652	2 I39811	parasporal crystal
4	2307.5	67.7	659	2 S10228	parasporal crystal
5	1178	34.6	719	2 I40590	crystal -
6	1156	33.9	719	2 I39815	insecticidal prote
7	1152.5	33.8	1138	2 A48944	parasporal crystal
8	1149	33.7	1157	1 S49247	parasporal crystal
9	1147	33.7	719	2 S25383	parasporal crystal
10	1147	33.7	719	2 I39814	insecticidal prote
11	1109	32.6	1228	2 S00873	parasporal crystal
12	1034.5	30.4	1160	2 I40569	parasporal crystal
13	988	29.0	1154	2 S39536	parasporal crystal
14	980	28.8	1155	2 A26513	parasporal crystal
15	980	28.8	1155	2 J00002	parasporal crystal
16	980	28.8	1156	2 A29125	parasporal crystal
17	971.5	28.5	1181	2 A41052	parasporal crystal
18	969	28.4	1155	2 I39838	parasporal crystal
19	967	28.4	1155	2 S02134	parasporal crystal
20	954.5	28.0	934	2 A22798	parasporal crystal
21	948.5	27.8	1176	2 J02041	parasporal crystal
22	944.5	27.7	655	2 J07140	protoxin - Bacillu
23	943.5	27.7	1176	2 J02219	parasporal crystal
24	943.5	27.6	1176	2 A22617	parasporal crystal
25	938.5	27.6	1176	2 S02215	parasporal crystal
26	937.5	27.5	1189	2 S00944	parasporal crystal
27	929.5	27.3	1176	2 A48970	parasporal crystal
28	912.5	26.8	823	2 S04181	parasporal crystal
29	911.5	26.8	1166	2 S32645	parasporal crystal

30	895.5	26.3	1156	2 A29838	parasporal crystal
31	883.5	25.9	1174	2 A42459	parasporal crystal
32	883	25.9	1171	2 A37829	parasporal crystal
33	883	25.9	1171	2 I40572	parasporal crystal
34	882	25.9	1174	2 S32649	parasporal crystal
35	852	25.0	1165	2 S11446	parasporal crystal
36	847	24.9	1177	2 A49785	parasporal crystal
37	845.5	24.8	1178	2 USB5X8	parasporal crystal
38	841	24.7	618	2 S11445	parasporal crystal
39	835.5	24.5	1160	2 S32647	parasporal crystal
40	820	24.1	1172	2 S32689	parasporal crystal
41	804	20.7	1380	2 B42459	hypothetical prote
42	677.5	19.6	1156	2 S19306	parasporal crystal
43	663	19.5	1136	1 USB581	parasporal crystal
44	626	18.4	934	2 B29838	parasporal crystal
45	617	18.1	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

A27323 parasporal crystal protein cry3aa1 - Bacillus thuringiensis

N:Alternate names: coleopteran-specific insect control protein; crystal protein cryC;

C/Species: Bacillus thuringiensis

C/Date: 19-Nov-1988 #sequence, revision 19-Nov-1988 #text-change 01-Dec-2000

C/Accession: A27323; A26853; A29987; A28407; S60781; I39812; I39813

R:Herrnstadt, C.; Gilroy, T.E.; Sobleski, D.A.; Bennett, B.D.; Gaertner, F.H.

Gene 57, 37-46, 1987

A/Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active

A/Reference number: A27323; MUID:88112860; PMID:2828180

A/Accession: A27323

A/Molecule type: DNA

A/Residues: 1-652 <HR>

A/Cross-references: GB:M22472; NID:G142733; PIDN:AAA22336.1; PID:G142734

A/Experimental source: strain San Diego

R:Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.

Nucleic Acids Res. 15, 7183, 1987

A/Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus t

A/Reference number: A26853; MUID:88015559; PMID:3658680

A/Accession: A26853

A/Molecule type: DNA

A/Residues: 9-652 <HO>

A/Cross-references: GB:Y00420; NID:940252; PIDN:CAA6482.1; PID:940253

A/Experimental source: var. tenebrionis

R:McPherson, S.A.; Perlak, F.J.; Fuchs, R.L.; Marrone, P.G.; Lavrik, P.B.; Fischhoff,

Bio/Technology 6, 61-66, 1988

A/Title: Characterization of the coleopteran-specific protein gene of Bacillus thurin

A/Reference number: A29987

A/Accession: A29987

A/Molecule type: DNA

A/Residues: 9-652 <MCP>

A/Experimental source: var. tenebrionis

R:Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987

A/Title: Molecular cloning and characterization of the insecticidal crystal protein 9

A/Reference number: A28407

A/Accession: A28407

A/Molecule type: DNA

A/Residues: 9-652 <SRK>

A/Experimental source: var. Tenebrionis

R:Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.

Mol. Microbiol. 14, 381-389, 1994

A/Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized stra

A/Reference number: S60781; MUID:95131759; PMID:7830581

A/Accession: S60781

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 9-652 <ADA>

A/Cross-references: EMBL:U10985; NID:9506182; PIDN:AMC43266.1; PID:9514312

A/Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

R:Wu, S.J.; Dean, D.H.
J. Mol. Biol. 255, 628-640, 1996
A:Title: Functional significance of loops in the receptor binding domain of Bacillus thuringiensis
A:Reference number: 562317; MUID:96163555; PMID:8568902
A:Contents: annotation

R:Donovan, W.P.; Gonzalez, J.M.
Mol. Gen. Genet. 214, 365-372, 1998

A:Title: Isolation and characterization of Eg2158, a new strain of Bacillus thuringiensis
A:Reference number: 139812; MUID:89112139; PMID:3146015

A:Accession: I39812

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 9-652 <RES>

A:Cross-references: GB:W37207; NID:9142735; PIDN:AAA50255.1; PID:9142736

A:Experimental source: strain Eg2158

R:Reisner, M.; Lecadet, M.M.; Lecadet, M.M.; Lecadet, M.M.
J. Bacteriol. 175, 2952-2960, 1993

A:Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a

A:Reference number: 139813; MUID:9323939; PMID:8491716

A:Accession: I39813

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 9-58 <RES>

A:Cross-references: GB:103393; NID:9304150; PIDN:AAA22350.1; PID:9551698

A:Gene: cryIIIA

A:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 100.0%; Score 3406; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 60
DB 9 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 68
QY 61 TTKDVIQKIGSVYDGLGVGPPFGALVSYTFNLTNPESDEPKAFMEQVEALMDOK 120
DB 69 TTKDVIQKIGSVYDGLGVGPPFGALVSYTFNLTNPESDEPKAFMEQVEALMDOK 128
QY 121 IADYAKKALAELOGLNQNNVEDYVSALSSQKNPVSSRNPHSGRIRRELSQASHEFRNS 180
DB 129 IADYAKKALAELOGLNQNNVEDYVSALSSQKNPVSSRNPHSGRIRRELSQASHEFRNS 188
QY 181 MPEFASISYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240
DB 189 MPEFASISYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 248
QY 241 DHCVKWYNGDLKLRGSSYESVWNNFRREMTLVLDLALFPLXYDVRRLYKREKTELT 300
DB 249 DHCVKWYNGDLKLRGSSYESVWNNFRREMTLVLDLALFPLXYDVRRLYKREKTELT 308
QY 301 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIQFHTRFQPGYGNDSFNWYS 360
DB 309 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIQFHTRFQPGYGNDSFNWYS 368
QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 420
DB 369 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 428
QY 421 KVEFSQYNDQDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 480
DB 429 KVEFSQYNDQDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 488
QY 481 MGSAGTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVAGPFTGGDIIOC 540
DB 489 MGSAGTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVAGPFTGGDIIOC 548
QY 541 TENGAATITVTPDVSQKRYRARIHYASTOITFTLSDAPFNQYFDKTIKNGDTLT 600
DB 549 TENGAATITVTPDVSQKRYRARIHYASTOITFTLSDAPFNQYFDKTIKNGDTLT 608

```

QY 601 YNSFNLASSTPELSEGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 609 YNSFNLASSTPELSEGNLQIGVTGLSAGDKVYIDKIEFIPVN 652

RESULT 2

JH0261

Parasporal crystal protein cry3cal - Bacillus thuringiensis subsp. kurstaki (strain B)

N/Alternate names: parasporal crystal protein cryIIID

C:Species: Bacillus thuringiensis subsp. kurstaki

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000

C:Accession: JH0261; S18944

R:Amber, B.; Theunis, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Se

Gene 110, 131-132, 1992

A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crys

A:Reference number: JH0261; MUID:92184108; PMID:1544571

A:Accession: JH0261

A:Molecule type: DNA

A:Residues: 1-649 <LAM>

A:Cross-references: EMBL:X59797; NID:940287; PIDN:CAA42469.1; PID:940288

A:Gene: cryIIID

A:Superfamily: parasporal crystal protein

Query Match 75.3%; Score 2564.5; DB 1; Length 649;
Best Local Similarity 74.4%; Pred. No. 4.3e-161;
Matches 485; Conservative 63; Mismatches 93; Indels 11; Gaps 5;

```

QY 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTENNEVPTNHVOYPLAETPNPTLEDLNTKEFLMTADNNTALDSS 58
QY 61 TTKDVIQKIGSVYDGLGVGPPFGALVSYTFNLTNPESDEPKAFMEQVEALMDOK 120
DB 59 TTKDVIQKIGSVYDGLGVGPPFGALVSYTFNLTNPESDEPKAFMEQVEALMDOK 118
QY 121 IADYAKKALAELOGLNQNNVEDYVSALSSQKNPVSSRNPHSGRIRRELSQASHEFRNS 180
DB 119 IADYAKKALAELOGLNQNNVEDYVSALSSQKNPVSSRNPHSGRIRRELSQASHEFRNS 178
QY 181 MPEFASISYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 240
DB 179 MPEFASISYEVLFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQEYT 238
QY 241 DHCVKWYNGDLKLRGSSYESVWNNFRREMTLVLDLALFPLXYDVRRLYKREKTELT 300
DB 239 DHCVKWYNGDLKLRGSSYESVWNNFRREMTLVLDLALFPLXYDVRRLYKREKTELT 298
QY 301 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIQFHTRFQPGYGNDSFNWYS 360
DB 299 RQVLTDPVIGVNNLNGYGTTFNSNIENYIRKPHLFYDLHRIQFHTRFQPGYGNDSFNWYS 358
QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 420
DB 359 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 418
QY 416 YSGTKEFSQYNDQDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 475
DB 419 YSGTKEFSQYNDQDEASTQYTDSCRNGAVSMDSIDLPETDEPLEKYSQHLANTVMKFL 478
QY 476 YMCFLMGSGKGTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVAGPFTGG 535
DB 479 YMCFLMGSGKGTIPVLTWTHKSVDFENMIDSKRITOLPLVKAYKLGSGASVAVAGPFTGG 538
QY 536 DIIOCTENGSAATITVTPDVSQKRYRARIHYASTOITFTLSDAPFNQYFDKTIKNGDTLT 593
DB 539 DIIOCTENGSAATITVTPDVSQKRYRARIHYASTOITFTLSDAPFNQYFDKTIKNGDTLT 597
QY 594 NKGDITLYNSFNLASSTPELSEGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 598 NKGDITLYNSFNLASSTPELSEGNLQIGVTGLSAGDKVYIDKIEFIPVN 649

```

RESULT 3

139811

parapsoral crystal protein cry3Bb1 - *Bacillus thuringiensis*

N/Alternate names: parapsoral crystal protein cryIIIB2

C/Species: *Bacillus thuringiensis*

C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000

C/Accession: I39811

R/Donovan, W.P.; Ruppert, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.H.

Appl. Environ. Microbiol. 58, 3921-3927, 1992

A/Title: Characterization of two genes encoding *Bacillus thuringiensis* insecticidal crys

A/Reference number: I39811; MUID:93119147; PMID:1476436

A/Accession: I39811

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-652 <RES>

A/Cross-references: GB:M89794; NID:g142729; PIDN:AAA2334.1; PID:g142730

C/Genetics:

A/Gene: cryIIIB2

C/Superfamily: parapsoral crystal protein

Query Match

Best Local Similarity 68.7%; Score 2341.5; DB 2; Length 652;

Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;

```

OY 1 MNPNNSEHDITKTENNEVPNNHVOYPLAETPNPLEDINYEFLRMADNTEALDSS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNPNNSEHDITKTENNEVPNNHVOYPLAETPNPLEDINYEFLRMADNTEALDSS 60
OY 61 TTKDVIQKISVYVDLLGVGVPFGALVSFYTNFLNTIWPSE-DPKAFMEQVLEALMDQ 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TVKAVAGTISVYQGLIGVGVFPAGALTSFYOSFLNTIWPSEDPKAFMAQVEVLIDK 120
OY 120 KIADYAKNKALAELOGLONNVEDYVSAISSQKNPVSRRNPSSQGRITRELSQASHFRN 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KIEEYAKSKALAELOGLONNVEDYVSAISSQKNPVSRRNPSSQGRITRELSQASHFRN 180
OY 180 SMPFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SMPFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 240
OY 240 TDHCVMYNNVGLDKLSSVSVNRRNRRREMTLVLDLALFPLVDVRLPKYKTEL 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TDHCVMYNNVGLDKLSSVSVNRRNRRREMTLVLDLALFPLVDVRLPKYKTEL 300
OY 300 TRDVLDPPIVGNLNGYGTFSNIENYIRKPHLFDYLHRIQFHTROPQGYGNDSEFNW 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TRDVLDPPIVGNLNGYGTFSNIENYIRKPHLFDYLHRIQFHTROPQGYGNDSEFNW 360
OY 360 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPSA-VYSG 418
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPSA-VYSG 420
OY 419 VTKVEFSQYNDQDEASTQYDSKRNVGAVS-WDSIDQLPETTDEPLEKYSHQNLNVM 477
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 VTKVEFSQYNDQDEASTQYDSKRNVGAVS-WDSIDQLPETTDEPLEKYSHQNLNVM 480
OY 478 CFMLQSGRGTIPVLTWTHKSVDFENMDSKKITQLPLVKAAYKLGASVAVAGPRFTGDI 537
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 CFMLQSGRGTIPVLTWTHKSVDFENMDSKKITQLPLVKAAYKLGASVAVAGPRFTGDI 540
OY 538 IQCTE-NGSAATVYT-PDVSYSOKYRARHAYASTOITFLLSDGAFENQYFEDKTIK 595
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 LFKSSNSIAKFEVTLNSAALLQRYRIRASTTNRLFVONSNDPLVYIINKTKNK 600
OY 596 GDTLTYSFNLASFPFELSG--NNLQIGVTGASAGDKYIIDKIEFIPV 643
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 DDDLTYQFDFLATNSNMGFSGDKNELIIGAESFVSNKITYIDKIEFIPV 650

```

RESULT 4

S10228

parapsoral crystal protein cry3ba1 - *Bacillus thuringiensis* (fragment)

N/Alternate names: coleopterian-active parapsoral crystal protein; delta-endotoxin

C/Species: *Bacillus thuringiensis*

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Dec-2000

C/Accession: S10228

R/Sick, A.; Gaertner, F.; Wong, A.

Nucleic Acids Res. 18, 1305, 1990

A/Title: Nucleotide sequence of a coleopterian-active toxin gene from a new isolate of

A/Reference number: S10228; MUID:90206811; PMID:2320431

A/Accession: S10228

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-659 <SIC>

A/Cross-references: EMBL:X17123; NID:g40256; PIDN:CAA3983.1; PID:g40259

C/Genetics:

A/Gene: cryIIIB

C/Superfamily: parapsoral crystal protein

C/Keywords: delta-endotoxin; toxin

Query Match

Best Local Similarity 67.7%; Score 2307.5; DB 2; Length 659;

Matches 442; Conservative 75; Mismatches 126; Indels 7; Gaps 6;

```

OY 1 MNPNNSEHDITKTENNEVPNNHVOYPLAETPNPLEDINYEFLRMADNTEALDSS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 MNPNNSEHDITKTENNEVPNNHVOYPLAETPNPLEDINYEFLRMADNTEALDSS 68
OY 61 TTKDVIQKISVYVDLLGVGVPFGALVSFYTNFLNTIWPSE-DPKAFMEQVLEALMDQ 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 TVKAVAGTISVYQGLIGVGVFPAGALTSFYOSFLNTIWPSEDPKAFMAQVEVLIDK 128
OY 120 KIADYAKNKALAELOGLONNVEDYVSAISSQKNPVSRRNPSSQGRITRELSQASHFRN 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 KIEEYAKSKALAELOGLONNVEDYVSAISSQKNPVSRRNPSSQGRITRELSQASHFRN 188
OY 180 SMPFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 189 SMPFAISGEVLEFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQY 248
OY 240 TDHCVMYNNVGLDKLSSVSVNRRNRRREMTLVLDLALFPLVDVRLPKYKTEL 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 TDHCVMYNNVGLDKLSSVSVNRRNRRREMTLVLDLALFPLVDVRLPKYKTEL 308
OY 300 TRDVLDPPIVGNLNGYGTFSNIENYIRKPHLFDYLHRIQFHTROPQGYGNDSEFNW 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 309 TRDVLDPPIVGNLNGYGTFSNIENYIRKPHLFDYLHRIQFHTROPQGYGNDSEFNW 368
OY 360 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPSA-VYSG 418
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 SGNVSTRPSIGSNDITSPFYGNKSSPEVONLENGEKYRAVANINLAWPSA-VYSG 428
OY 419 VTKVEFSQYNDQDEASTQYDSKRNVGAVS-WDSIDQLPETTDEPLEKYSHQNLNVM 477
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 429 VTKVEFSQYNDQDEASTQYDSKRNVGAVS-WDSIDQLPETTDEPLEKYSHQNLNVM 488
OY 478 CFMLQSGRGTIPVLTWTHKSVDFENMDSKKITQLPLVKAAYKLGASVAVAGPRFTGDI 537
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 489 CFMLQSGRGTIPVLTWTHKSVDFENMDSKKITQLPLVKAAYKLGASVAVAGPRFTGDI 548
OY 538 IQCTE-NGSAATVYT-PDVSYSOKYRARHAYASTOITFLLSDGAFENQYFEDKTIK 595
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 549 LFKSSNSIAKFEVTLNSAALLQRYRIRASTTNRLFVONSNDPLVYIINKTKNK 608
OY 596 GDTLTYSFNLASFPFELSG--NNLQIGVTGASAGDKYIIDKIEFIPV 643
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 609 DDDLTYQFDFLATNSNMGFSGDKNELIIGAESFVSNKITYIDKIEFIPV 658

```

RESULT 5

I40590

cry465 protein - *Bacillus thuringiensis*

C/Species: *Bacillus thuringiensis*

C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999

C/Accession: I40590

R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A:Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis* tomocoids.

A:Reference number: I39814; MUID:95314293; PMID:7793960

A:Accession: I40590

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: EMBL:U07642; NID:g467234; PID:AAA8211.1; PID:g467235

A:Gene: cryV465

A:Superfamily: parasporal crystal protein

Query Match 34.6%; Score 1178; DB 2; Length 719;
 Best Local Similarity 38.6%; Pred. No. 1.1e-69;

Matches 256; Conservative 132; Mismatches 234; Indels 42; Gaps 15;

```

QY 1 MNPNNRSEHDTIKTEN-NEVPTNHVOYPLAETPPT---LEDLNYKEFLMTADNNTA 56
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLLKNDPKHOSLSMAKVDKIDTSLK-----NETDIELKNNHEDCLMSEYENP 50
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1 DSSSTFADVIQKGISVVDLLGVGFPFGALVSPYTNFLNTIWP-SDDPKAKMEQVEA 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 51 IDPFVASTIGTIGIAGKLTGLGVPFAGQIASLSFSLGELMPKKGKQMEIEMEHEE 110
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LMDQKIDYAKKALAELOGANNVEDYVSALSMQKNPVSSRNPHSGRIREFSQAES 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 IINOKITLYARKNALSLDGLDALAVYHDSLESWEN--RNNTARASVVKQYIALEL 167
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 HFRNSPFAISGVEVLEFLTYAQAANTHFLDKAOIYGEEMGYEKEDIAEYKROKL 235
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 MFVQKLPSPFAVSGEVEPLPIYAQAANHLHLLDASIFGEMKLSSEISTFTNNROYER 227
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 TOEYDHCYKMYNGLDKLGRSSYESWVNNRNRREMTLVLDLALFPLYDVALPKREV 295
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 TRDYSDHCYKMYNGLDKLGRSSYESWVNNRNRREMTLVLDLALFPLYDVALPKREV 287
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 296 KTELTDVLDPIVGVNMLRGYGT-----FSNIE-NYIKRPHLEFDYLRHIOFH-- 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TSQLTREYVTDALGVHPQAFASITWYNNAPSFSAIEAAVIRSPHLLDFLEKVIYSL 347
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 -TRFOPGYGNDNFYNSGNYSTRPSIGSNDITSPFYGNKSSPEYONLENGEKYRA 402
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 LSRMSNTQY----MMMGHRLER-RTIGTLNISTGSTNTSINP-TLPFSRDVYRT 401
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 403 VANTNLAVPSAVYSGVTKVEFS-QYNDQDEASTQYIDSKRNVGAVSMISDQLPEPTT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 402 ESTLAGLNLFLTOPVNGVPRVDFHMKFPTLPFIASDNFYLGAGVGTQLDSENELPEPT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 DEPLEKGYSHQNLNYVCMFLMOGSRGTIPVLWTWTHKSVDFNMIDSKKITQLPLVYAKYKQ 521
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 462 GQPVYESYSHRLSHI--GLISASHVKALVYSWTHRSADRTNTEPNSTIQIPLVAFNLS 519
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 522 SCASVAVAGPRTGGDIIOCTENGSAATYVTPDVYSQYKRRARIHYASTSQITFTLSLDG 581
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 520 SGAAYVVRGPGTGGDILRRNTGTGGDIRVNNINPFAQRVRIYASTTDLDFHTSING 579
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 APFNQYFEDKTIINKGDTLYNSFNLSASTPELGS--NNLQIGVYGLSAGDKVYIDKIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 580 KAINQGNFSATMNGEDLDYKTFRTIGFTTFSFSDVOSTFTIGAMNFSGNGEYIDRIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 6

I39815

Insecticidal protein cryV - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*

C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999

C:Accession: I39815

R:Gleave, A.P.; Williams, R.; Hedges, R.J.

Appl. Environ. Microbiol. 59, 1683-1687, 1993
 A:Title: Screening by polymerase chain reaction of *Bacillus thuringiensis* serotypes f

lensis subsp. kurstaki.

A:Reference number: I39815; MUID:93298009; PMID:8517758

A:Accession: I39815

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: GB:M98544; NID:g142767; PID:AAA22354.1; PID:g142768

A:Gene: cryV

A:Superfamily: parasporal crystal protein

Query Match 33.9%; Score 1156; DB 2; Length 719;
 Best Local Similarity 38.0%; Pred. No. 3.2e-68;

Matches 252; Conservative 132; Mismatches 238; Indels 42; Gaps 15;

```

QY 1 MNPNNRSEHDTIKTEN-NEVPTNHVOYPLAETPPT---LEDLNYKEFLMTADNNTA 56
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLLKNDPKHOSLSMAKVDKIDTSLK-----NETDIELKNNHEDCLMSEYENP 53
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 LSSSTFADVIQKGISVVDLLGVGFPFGALVSPYTNFLNTIWP-SDDPKAKMEQVEA 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 54 FVFAST---IGTIGIAGKLTGLGVPFAGQVASLSFSLGELMPKKGKQMEIEMEHEE 110
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 LMDQKIDYAKKALAELOGANNVEDYVSALSMQKNPVSSRNPHSGRIREFSQAES 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 IINOKITLYARKNALSLDGLDALAVYHDSLESWEN--RNNTARASVVKQYIALEL 167
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 HFRNSPFAISGVEVLEFLTYAQAANTHFLDKAOIYGEEMGYEKEDIAEYKROKL 235
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 MFVQKLPSPFAVSGEVEPLPIYAQAANHLHLLDASIFGEMKLSSEISTFTNNROYER 227
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 TOEYDHCYKMYNGLDKLGRSSYESWVNNRNRREMTLVLDLALFPLYDVALPKREV 295
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 AGDYSYDHCYKMYNGLDKLGRSSYESWVNNRNRREMTLVLDLALFPLYDVALPKREV 287
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 296 KTELTDVLDPIVGVNMLRGYGT-----FSNIE-NYIKRPHLEFDYLRHIOFH-- 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TSQLTREYVTDALGVHPHPSFTTWYNNAPSFSAIEAAVIRNPHLLDFLEQVITYSL 347
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 -TRFOPGYGNDNFYNSGNYSTRPSIGSNDITSPFYGNKSSPEYONLENGEKYRA 402
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 LSRMSNTQY----MMMGHRLER-RTIGTLNISTGSTNTSINP-TLPFSRDVYRT 401
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 403 VANTNLAVPSAVYSGVTKVEFS-QYNDQDEASTQYIDSKRNVGAVSMISDQLPEPTT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 402 ESTLAGLNLFLTOPVNGVPRVDFHMKFVTHPIASDNFYLGAGVGTQLDSENELPEPT 461
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 DEPLEKGYSHQNLNYVCMFLMOGSRGTIPVLWTWTHKSVDFNMIDSKKITQLPLVYAKYKQ 521
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 462 GQPVYESYSHRLSHI--GLISASHVKALVYSWTHRSADRTNTEPNSTIQIPLVAFNLS 519
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 522 SCASVAVAGPRTGGDIIOCTENGSAATYVTPDVYSQYKRRARIHYASTSQITFTLSLDG 581
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 520 SGAAYVVRGPGTGGDILRRNTGTGGDIRVNNINPFAQRVRIYASTTDLDFHTSING 579
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 582 APFNQYFEDKTIINKGDTLYNSFNLSASTPELGS--NNLQIGVYGLSAGDKVYIDKIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 580 KAINQGNFSATMNGEDLDYKTFRTIGFTTFSFSDVOSTFTIGAMNFSGNGEYIDRIE 639
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 FIVP 643
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7

A48944

Parasporal crystal protein cry7Aa1 - *Bacillus thuringiensis*

N:Alternate names: parasporal crystal protein cry7IIC

C:Species: *Bacillus thuringiensis*

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A48944

C:Accession: S25383
 R:Taylor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
 Mol. Microbiol. 6, 1211-1217, 1992
 A:Title: Identification and characterization of a novel *Bacillus thuringiensis* delta-end
 A:Reference number: S25383; MID:92269582; PMID:1588820
 A:Accession: S25383
 A:Molecule type: DNA
 A:Residues: 1-719 <TAI>
 A:Cross-references: EMBL:X62821; NID:940289; PID:CAA44633.1; PID:940290
 C:Genetics:
 A:Gene: cryV
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 33.7%; Score 1147; DB 2; Length 719;
 Best Local Similarity 37.8%; Pred. No. 1.2e-67;
 Matches 251; Conservative 132; Mismatches 239; Indels 42; Gaps 15;

QY 1 MNRNREHDTIKTTER-NEVPTNHVOYPLAETPPT---LEDLNYKEFLRMTADNNTA 56
 DB 1 MKLRNDKHQSFSSNAKVDKISTDSLK-----NETDIELQNIHEDCLKSEYENVEP 53
 QY 57 LDSSTKDYIOKGISVGDLLGVGFPFGALVSEYTNFLNTIMP-SEDPKAFMEQVEA 115
 DB 54 FVSAST---IQGIGIAGKILGTLGVFPAGVASLSFLLGELMPKGNOMEIEMHEVEE 110
 QY 116 LMDOKIADYAKNKALAELOGQNNVEDYVSLSSMOKNPVSSRNPHSGRIRLEFSQAES 175
 DB 111 IINOKISTYARKKALTDLKGDLALVYHDSLESVGN--RNNTARASVYKSYQYILEL 167
 QY 176 HERNMSPFSAISGYEVLFLTYAQAANTHLFLKDAQIYGEKGEKEDIAEFKROKL 235
 DB 168 MEVQKLPSPFASGEVPLPIYAQAANHLHLLDASIFGKEMGLSSSEISTEYFNQVER 227
 QY 236 TOETDHCYKMYNGGLKRGSSSESVNENRYRREMTLVLDLALFPLYDVALPKREV 295
 DB 228 AGDYSYHCYKMYSTGLNLRGTNAESWVRYNQFRDMTLWLDLALFPLYDVALPKREV 287
 QY 296 KTELTDVLDPIYGVNRLRGYTT-----FSNIE-NYIKRPHLYLHRIQFH-- 343
 DB 288 TAOITREYTTALGIVHHPSPFTSTWYNNNAPEFSAIEAAVVRPHLDLFLQVYISL 347
 QY 344 -TRQPGYVGNDSFNWYSGNVSTRPSIGNDITSPFYGNKSSPEYQONLENGEKYRA 402
 DB 348 LSRMSNTQY---NMWNGHKLFR-TIGGLNISTQGSTNINPV-TLPFTSRDYKRT 401
 QY 403 VANTNLAVPSPAVYSGVTKVEFS-QYNDQDEASTQTYDSKRNAGAVSWSIDQLPETT 461
 DB 402 ESLAGINLFLTQPVNGVPRVDFHMKFVTHPIASDNPFYVPGYAGIGTQLODSSENLPEAT 461
 QY 462 DEPLEKGYSHQNLVWCFIMOGSRGTIPVLTWTHKSVDFFNMIDSKITQDPLVAKYKQ 521
 DB 462 GQPNYESHSLSHI--GLISASHVAKALVSWTHRSADRNTIEPNSITQDPLVAKFNL 519
 QY 522 SGASVAVAPREFGDIIOCTENGSAATIVTPDVYSOKYRARIHVASQITFTSLDG 581
 DB 520 SGAAYVVRGPGFTGGDILRTNTGTGDIRVNNPFAQRYRIRASTIDIOFTSING 579
 QY 582 APFNOYFEDKTIKNGDILTYNSFNLASFPFELS--NNLOIGVGLSAGDYYIDKIE 639
 DB 580 KAIQGNFSATMNGEDLDYKTFRTVGFTEPFSFLDVOSTFTIGAMNFSGNEVYIDRIE 639
 QY 640 FIPV 643
 DB 640 FVPV 643

RESULT 10
 139814
 Insecticidal protein cryVI - *Bacillus thuringiensis*
 C:Species: *Bacillus thuringiensis*
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C:Accession: 139814

R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A:Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis*
 A:Reference number: 139814; MID:95314293; PMID:7793960
 A:Accession: 139814
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-719 <RES>
 A:Cross-references: GB:L36338; NID:9540281; PID:AA036999.1; PID:9540282
 C:Genetics:
 A:Gene: cryVI
 C:Superfamily: parasporal crystal protein

Query Match 33.7%; Score 1147; DB 2; Length 719;
 Best Local Similarity 37.8%; Pred. No. 1.2e-67;
 Matches 251; Conservative 132; Mismatches 239; Indels 42; Gaps 15;

QY 1 MNRNREHDTIKTTER-NEVPTNHVOYPLAETPPT---LEDLNYKEFLRMTADNNTA 56
 DB 1 MKLRNDKHQSFSSNAKVDKISTDSLK-----NETDIELQNIHEDCLKSEYENVEP 53
 QY 57 LDSSTKDYIOKGISVGDLLGVGFPFGALVSEYTNFLNTIMP-SEDPKAFMEQVEA 115
 DB 54 FVSAST---IQGIGIAGKILGTLGVFPAGVASLSFLLGELMPKGNOMEIEMHEVEE 110
 QY 116 LMDOKIADYAKNKALAELOGQNNVEDYVSLSSMOKNPVSSRNPHSGRIRLEFSQAES 175
 DB 111 IINOKISTYARKKALTDLKGDLALVYHDSLESVGN--RNNTARASVYKSYQYILEL 167
 QY 176 HERNMSPFSAISGYEVLFLTYAQAANTHLFLKDAQIYGEKGEKEDIAEFKROKL 235
 DB 168 MEVQKLPSPFASGEVPLPIYAQAANHLHLLDASIFGKEMGLSSSEISTEYFNQVER 227
 QY 236 TOETDHCYKMYNGGLKRGSSSESVNENRYRREMTLVLDLALFPLYDVALPKREV 295
 DB 228 AGDYSYHCYKMYSTGLNLRGTNAESWVRYNQFRDMTLWLDLALFPLYDVALPKREV 287
 QY 296 KTELTDVLDPIYGVNRLRGYTT-----FSNIE-NYIKRPHLYLHRIQFH-- 343
 DB 288 TAOITREYTTALGIVHHPSPFTSTWYNNNAPEFSAIEAAVVRPHLDLFLQVYISL 347
 QY 344 -TRQPGYVGNDSFNWYSGNVSTRPSIGNDITSPFYGNKSSPEYQONLENGEKYRA 402
 DB 348 LSRMSNTQY---NMWNGHKLFR-TIGGLNISTQGSTNINPV-TLPFTSRDYKRT 401
 QY 403 VANTNLAVPSPAVYSGVTKVEFS-QYNDQDEASTQTYDSKRNAGAVSWSIDQLPETT 461
 DB 402 ESLAGINLFLTQPVNGVPRVDFHMKFVTHPIASDNPFYVPGYAGIGTQLODSSENLPEAT 461
 QY 462 DEPLEKGYSHQNLVWCFIMOGSRGTIPVLTWTHKSVDFFNMIDSKITQDPLVAKYKQ 521
 DB 462 GQPNYESHSLSHI--GLISASHVAKALVSWTHRSADRNTIEPNSITQDPLVAKFNL 519
 QY 522 SGASVAVAPREFGDIIOCTENGSAATIVTPDVYSOKYRARIHVASQITFTSLDG 581
 DB 520 SGAAYVVRGPGFTGGDILRTNTGTGDIRVNNPFAQRYRIRASTIDIOFTSING 579
 QY 582 APFNOYFEDKTIKNGDILTYNSFNLASFPFELS--NNLOIGVGLSAGDYYIDKIE 639
 DB 580 KAIQGNFSATMNGEDLDYKTFRTVGFTEPFSFLDVOSTFTIGAMNFSGNEVYIDRIE 639
 QY 640 FIPV 643
 DB 640 FVPV 643

RESULT 11
 S00873
 parasporal crystal protein cryBa1 - *Bacillus thuringiensis* subsp. *thuringiensis*
 N:Alternate names: parasporal crystal protein cryA4
 C:Species: *Bacillus thuringiensis* subsp. *thuringiensis*
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000

C:Accession: S00873
R:Brizard, B.L., Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A>Title: Nucleotide sequence of an additional crystal protein gene cloned from *Bacillus*
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:CROSS-references: EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PTD:g580949
C:Genetics:
A:Gene: cryA4
A:Start codon: TTTG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 32.6%; Score 1109; DB 2; Length 1228;
Best Local Similarity 38.3%; Pred. No. 9, 1e-65;
Matches 256; Conservative 116; Mismatches 237; Indels 60; Gaps 22;

OY 1 MPNNRSEHDTIKTEENNVPPTNHQYPLAEHPNPLEDLNKEFLMTADNNTLEALDSS 60
DB 1 MNSNRKNEHEIINAVSNHSAQND-----LLPARIEDSICIAEGNNDPFVSA 48
OY 61 TTAKDIQAGISVAYGDLLGYVFPFGALVSFTYNFNLTIMP--SEDPMKAMEQVEALMD 119
DB 49 ST---VQTINIGRIQLGVGFPAQGLASFYSFLVGELMPKRGRDWEIFLEHEDLIHQ 105
OY 120 KTADVAKNKALDELQIGNVEDYVALSSMQKNPVSSRNPHSQGRIRE-LFSQ---AES 175
DB 106 QITENAKRNTALALQGLDSFRAYQOSLEDMLDN-----RDARKRSVLTYNQYALIEL 158
OY 176 HFENSMPFAISGISGEVLFETTVYAQAANTHLFLKDQAIYEEMKYEKEDIAPFKRKDKL 235
DB 159 DEFANAPLPFAIRNOEVPPLIMVYAQAANTHLILLRLDASLFFSESGELTSQEIQRYERQVER 218
OY 236 TOEYTHCYKMYWVNGLDKLGGSSYESWNPNRRYRREWTLYVDLIAFLPYDVARYKEYEV 295
DB 219 TRDYSDCVEMWNTGLNSLGTNAASWVRYNORFDLTGLVDLVAFPSYDFRTFYINT 278
OY 296 KTELTRDYLDPYI--VGVN--NLRGYGT---TESNIE-NYIRKPDLFDYLRHOFTTRFO 347
DB 279 SAQTLREVYTDAIGATGSVMNASMMWYNNNAPSFAIEAAAIRSPHLDFLEQLTIFSA-S 337
OY 348 PGYYGNDSPYWGCGNYSTRPSIGSNDLIITSPPFG--NKSESPQNLEFNCEKYYRAVAN 405
DB 338 SRMSNRHMHTYMGHTIQSRP-IIGG--LNTSHGANITSINPY-TLRFASRDYRRESY 393
OY 406 TNLAVMSPAY----SGVTVFESQYNDQ--TDEAS--TGTFYDSKRNVAGVSWDSIDL 456
DB 394 AGVILW--GIYLERIHGVPIYRFNFETNPONISDRGTANYSQLPESP--GLQKDSREL 448
OY 457 PPETTEDPLEKGYSHQUNTYMCFIAMOGSKGITPLYLTHKSVDFNMIDSKKIOLPYLK 516
DB 449 PPETTERPENESYSHRISHGIILQ--SRNVAPYSWHRADRNTNTGPNRITQIDIPWK 506
OY 517 AYKLOSASVAVAGRFTGDIIOCTENGSAATIIVTPDVSQKRYRARIHYASTQSOLTFT 576
DB 507 ASLELPQGITVYVRGGLFGDGLTRTNNGGFEPIRYTVGPIQRIRIGEFRASTVDPDFEF 566
OY 577 LSLDGADPNQYYPDKTIINKDPTLYNSFNLASFSITPEELS--GNMLQICVGLSGADKY 634
DB 567 VSRGCTVVNNRFLRFTMNSGDELKYGNFVRRAFETPTPETQIDIIRTSIGLSGNGEYV 626
OY 635 IDKIEPIYV 643
DB 627 IDKIEIIPV 635

RESULT 12
140589
parasporal crystal protein crysCal - *Bacillus thuringiensis*
N:Alternate names: parasporal crystal protein cryIII
C:Species: *Bacillus thuringiensis*

[illegible]

1000

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 10:45:44 : Search time 14 Seconds

(without alignments)
1907.911 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 3406

Sequence: 1 MNPNNRSEHDRIKTEENNEV.....TGLSAGDKVYIDKIEFIPVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3406	100.0	644	1 C3AA_BACTT	P07130 bacillus th
2	2564.5	75.3	649	1 C3CA_BACTK	Q45744 bacillus th
3	2341.5	68.7	652	1 C3BB_BACTU	Q06117 bacillus th
4	2307.5	67.7	659	1 C3BA_BACTO	P17969 bacillus th
5	1240	36.4	1157	1 C8AA_BACUK	Q45704 bacillus th
6	1187	34.9	1169	1 C8BA_BACUK	Q45705 bacillus th
7	1178	34.6	719	1 C1IB_BACTE	Q45709 bacillus th
8	1176.5	34.5	719	1 C1ID_BACTU	Q9X411 bacillus th
9	1174.5	34.5	1138	1 C7AB_BACUK	Q45708 bacillus th
10	1159.5	34.0	1138	1 C7AB_BACUA	Q45707 bacillus th
11	1156.5	34.0	1229	1 C1BB_BACTU	Q45739 bacillus th
12	1156.5	34.0	1233	1 C1BC_BACTM	Q45774 bacillus th
13	1156	33.9	719	1 C1IA_BACTK	Q45752 bacillus th
14	1152.5	33.8	1138	1 C7AA_BACTU	Q03749 bacillus th
15	1149	33.7	1157	1 C9CA_BACTO	Q45733 bacillus th
16	1141	33.5	1169	1 C9DA_BACTP	Q06014 bacillus th
17	1130.5	33.2	1215	1 C1KA_BACTM	Q45715 bacillus th
18	1109	32.6	1228	1 C1BA_BACTM	P05517 bacillus th
19	1090	32.0	719	1 C1IC_BACTU	Q87404 bacillus th
20	1063.5	31.2	1227	1 C1BE_BACTU	Q05805 bacillus th
21	1044.5	30.7	1150	1 C9EA_BACTA	Q9Z419 bacillus th
22	1034.5	30.4	1231	1 C8CA_BACTP	Q45706 bacillus th
23	1030.5	30.3	1231	1 C1BD_BACTZ	Q9Z425 bacillus th
24	1012.5	29.7	1163	1 C0AA_BACTF	Q9X597 bacillus th
25	980	28.8	1155	1 C1AB_BACTM	P06578 bacillus th
26	971.5	28.5	1181	1 C1AE_BACTL	Q03748 bacillus th
27	970	28.5	1179	1 C1AD_BACTA	Q03744 bacillus th
28	944.5	27.7	1189	1 C1CA_BACTE	P05518 bacillus th
29	938.5	27.6	1176	1 C1AA_BACTG	P02965 bacillus th
30	929.5	27.3	1176	1 C1CB_BACTG	P69563 bacillus th
31	926	27.2	1170	1 C1JB_BACTU	Q45716 bacillus th
32	920	27.0	1169	1 C1GB_BACTZ	Q9Z426 bacillus th
33	911.5	26.8	1166	1 C1GA_BACTU	Q45746 bacillus th

34	908.5	26.7	1167	1 C1JA_BACTU	Q45738 bacillus th
35	883.5	25.9	911	1 C1AF_BACTU	P96315 bacillus th
36	883.5	25.9	1174	1 C1FA_BACTA	Q03746 bacillus th
37	883	25.9	1171	1 C1EA_BACTM	Q57458 bacillus th
38	882	25.9	1169	1 C1FB_BACTM	Q66377 bacillus th
39	860.5	25.3	1174	1 C1EB_BACTA	Q03745 bacillus th
40	859.5	25.2	1176	1 C1AG_BACTU	Q98515 bacillus th
41	852	25.0	1165	1 C1AD_BACTA	P19415 bacillus th
42	845.5	24.8	1178	1 C1AC_BACTK	P50068 bacillus th
43	835.5	24.5	1160	1 C1DB_BACTU	Q45747 bacillus th
44	828	24.3	1155	1 C1HB_BACTM	Q45718 bacillus th
45	820	24.1	1172	1 C1HA_BACTU	Q45748 bacillus th

ALIGNMENTS

RESULT 1
ID C3AA_BACTT STANDARD: PRT: 644 AA.

AC P07130; P21255;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry3Aa precursor (insecticidal delta-endotoxin CryIIIA(a)) (crystalline entomocidal protoxin) (73 kDa crystal protein).
GN CRY3AA OR CRYIIIA(A) OR CRYIIA OR CRY3A OR CRYC OR BT13.
OS Bacillus thuringiensis (subsp. tenebrionis).
OS Bacillus thuringiensis (subsp. morrisoni), and
OS Bacillus thuringiensis (subsp. san diego).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1444, 1441, 1435;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RX MEDLINE=88015559; PubMed=3658680;
RA Hoeft H., Seurinck J., Houtven A.V., Vaack M.;
RT "Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";
RL Nucleic Acids Res. 15:7183-7183(1987).
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA Sekar V., Thompson D.V., Maroney M.J., Bookland R.G., Adang M.J.;
RT "Molecular cloning and characterization of the insecticidal crystal protein gene of Bacillus thuringiensis var. tenebrionis.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
[3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavrik P.B., Fischhoff D.A.;
RT "Characterization of the coleopteran-specific protein gene of Bacillus thuringiensis var. tenebrionis.";
RL Biotechnology 6:61-66(1988).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis; STRAIN=NB176;
RX MEDLINE=9511759; PubMed=7830581;
RA Adams L.F., Mathewes S., O'Hara P., Petersen A., Gurtler H.;
RT "Elucidation of the mechanism of CryIIIA overproduction in a mutant strain of Bacillus thuringiensis var. tenebrionis.";
RL Mol. Microbiol. 14:381-389(1994).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.morrisoni; STRAIN=EG2158;
RX MEDLINE=89112139; PubMed=316015;
RA Donovan W.P., Gonzalez J.M., Jr., Gilbert M.P., Dankocsik C.C.;
RT "Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis toxic to coleopteran larvae, and nucleotide sequence of the toxin gene.";
RL Mol. Gen. Genet. 214:365-372(1988).

RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES-B.t.san diego;
 RX MEDLINE-88112860; PubMed-2828180;
 RA Hermsdorf C., Gilroy T.E., Sobleski D.A., Bennett B.D.,
 RA Gaertner F.H.;
 RT "Nucleotide sequence and deduced amino acid sequence of a coleopteran-
 RT active delta-endotoxin gene from *Bacillus thuringiensis* subsp. *san*
 RT *diego*.";
 RL Gene 57:37-46(1987).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC SPECIES-B.t.tenebrionis;
 RX MEDLINE-92049729; PubMed-1658659;
 RA Li J., Carroll J.J., Ellar D.J.;
 RT "Crystal structure of insecticidal delta-endotoxin from *Bacillus*
 RT *thuringiensis* at 2.5-A resolution.";
 RL Nature 353:815-821(1991).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- BIOCHEMISTRY: Introduced by genetic manipulation and expressed in
 CC insect-resistant potato by Monsanto.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: Y00420; CAA68482.1; -
 DR EMBL: J02978; AAA22581.1; -
 DR EMBL: M37207; AAA50295.1; -
 DR EMBL: U10985; AAC43266.1; -
 DR EMBL: M30503; AAA22542.1; -
 DR EMBL: M22472; AAA22336.1; ALF_INIT.
 DR PIR: A26853; A26853.
 DR PIR: A28407; A28407.
 DR PIR: A29987; A29987.
 DR PIR: A27323; A27323.
 DR PDB: 1DLC; 30-SEP-94.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KM Toxin; Sporulation; 3D-structure; Genetically modified food.
 FT PROPEP 1 57 REMOVED IN MATURE FORM.
 FT CHAIN 58 644 PESTICIDIAL CRYSTAL PROTEIN CRY3AA.
 FT CONFLOC 544 544 G -> A (IN REF. 3).
 SQ SEQUENCE 644 AA; 73108 MW; EECFICEFD9683 CRC64;
 Query Match 100.0%; Score 3406; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 1,3e-216;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MNPNNRSHDTIKTENNEVPTNHQVPLAETPNPTLEDNLKKEFLRTADNTEALDSS 60
 Db 1 MNPNNRSHDTIKTENNEVPTNHQVPLAETPNPTLEDNLKKEFLRTADNTEALDSS 60
 Oy 61 TTKVOIGISVGDGLGVGFPFGGALVSFTYNTFLNTWSEDPKRAFMQVEALMDOK 120
 Db 61 TTKVOIGISVGDGLGVGFPFGGALVSFTYNTFLNTWSEDPKRAFMQVEALMDOK 120
 Oy 121 IADYAKNALAELOGLONNVEDYSAISSWQKNVSSRNPSQCRIRIELHSQASSHRNS 180
 Db 121 IADYAKNALAELOGLONNVEDYSAISSWQKNVSSRNPSQCRIRIELHSQASSHRNS 180
 Oy 181 MPSPALSGEVLFTTYAAANTHLFLKDAQIYGEEMGYEKEDIAEFYKQKLTDQET 240
 Db 181 MPSPALSGEVLFTTYAAANTHLFLKDAQIYGEEMGYEKEDIAEFYKQKLTDQET 240

Db 181 MPSPALSGEVLFTTYAAANTHLFLKDAQIYGEEMGYEKEDIAEFYKQKLTDQET 240
 Oy 241 DHCVKYNVGLDKLRSSYESWVNNRRYRRENTLVLDLALFPYDRLPKREKTELT 300
 Db 241 DHCVKYNVGLDKLRSSYESWVNNRRYRRENTLVLDLALFPYDRLPKREKTELT 300
 Oy 301 ROVLNDPIYGVNNLNGYGTTFENIENYIRKPLFYLHRIQPHRPOGYGNSFNWYS 360
 Db 301 ROVLNDPIYGVNNLNGYGTTFENIENYIRKPLFYLHRIQPHRPOGYGNSFNWYS 360
 Oy 361 GNYVSTRSIGSDNITTSPEYGNKSEPVONLEFNGEYKAVANTNLAVPSAVSGVT 420
 Db 361 GNYVSTRSIGSDNITTSPEYGNKSEPVONLEFNGEYKAVANTNLAVPSAVSGVT 420
 Oy 421 KYEFSQYNDQIDEASTQYDSKRNVAWSMDIDLPETDEPLEKGYSHQLYVMCF 480
 Db 421 KYEFSQYNDQIDEASTQYDSKRNVAWSMDIDLPETDEPLEKGYSHQLYVMCF 480
 Oy 481 MGSNGTIPVLTHKSYDFPMIDSKKITQLPLVKAKKLOGSASVAGPFTGDIIOC 540
 Db 481 MGSNGTIPVLTHKSYDFPMIDSKKITQLPLVKAKKLOGSASVAGPFTGDIIOC 540
 Oy 541 TENGSAATITVYPDVYSQKRYARIHYASTQITFTSLDGAPOYFPDKTINKGDTLT 600
 Db 541 TENGSAATITVYPDVYSQKRYARIHYASTQITFTSLDGAPOYFPDKTINKGDTLT 600
 Oy 601 YNSFNLASFSTPFELSGNNLQIGYTGAGDKYIKIEFIPIV 644
 Db 601 YNSFNLASFSTPFELSGNNLQIGYTGAGDKYIKIEFIPIV 644
 RESULT 2
 ID C3CA_BACTK STANDARD: PRT: 649 AA.
 AC 045744;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cry3Ca (insecticidal delta-endotoxin
 DE cryIII(c)) (crystalline entomocidal protoxin) (73 kDa crystal
 DE protein).
 GN CRY3CA OR CRYIII(C) OR CRYIID.
 OS *Bacillus thuringiensis* (subsp. *kurstaki*).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID-29339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BT1109P;
 RX MEDLINE-92184108; PubMed-1544571;
 RA Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C.,
 RA Janssens S., Seurlock J., Peferoen M.;
 RT "Nucleotide sequence of gene cryIId encoding a novel coleopteran-
 RT active crystal protein from strain BT1109P of *Bacillus thuringiensis*
 RT subsp. *kurstaki*.";
 RL Gene 110:131-132(1992).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: X59797: CAA42469.1: -
 DR HSSP: P07130: IDIC
 DR InterPro: IPR001178: Endotoxin.
 DR Pfam: PF00555: endotoxin.1.
 DR Toxin: Sporulation.
 KW SEQUENCE 649 AA: 73026 MW: 8FELF0B47957AC49 CRC64:

Query Match 75.3%: Score 2564.5; DB 1: Length 649;
 Best Local Similarity 74.4%: Pred. No. 36-161;
 Matches 465; Conservative 63; Mismatches 93; Indels 11; Gaps 5;

1 MNPNNRSEHDTIKTENNENPTNHNVOYPLAETNPPTLEDLNKKEFLRMADNTEALDSS 60
 1 MNPNNRSEHDTIKTENNENPTNHNVOYPLAETNPPTLEDLNKKEFLRMADNTEALDSS 58
 61 TTKDVIOKGISVVDLGIVGPPFGALVSFTYNTPLNTIPSPDPMKAFMEVQALMDOK 120
 59 TTKDAIOKGISIGDLGGVGFPGALVSFTYNTPLNTIPSPDPMKAFMEVQALMDOK 118
 121 IADYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSOGRIRELFQAESHFRNS 180
 119 IADYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSOGRIRELFQAESHFRNS 178
 181 MFSFAISGEVLEFLTYAQAANTHLEFLDKDAQYGEEMGEKEDIAEFYKROLKLOET 240
 179 MFSFAISGEVLEFLTYAQAANTHLEFLDKDAQYGEEMGEKEDIAEFYKROLKLOET 238
 241 DHCYKWNVGLDKLRGSSYSWNNENRYRREMTLTVDLIALFPYDVALYKREVKTELT 300
 239 NHCAKWKAKGLDLRGSTYEEMWKNRYRREMTLTVDLIALFPYDVALYKREVKTELT 298
 301 RDVLTDPYGVNNLRGTYGTFESNIENYIRKPHLEFDYLRHIOFTFRPOGYGNDSEFNYS 360
 299 RDVLTDPYGVNNLRGTYGTFESNIENYIRKPHLEFDYLRHIOFTFRPOGYGNDSEFNYS 358
 361 GNVYSTRPSIGSNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAV 415
 359 GNVYSTRPSIGSNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAV 418
 416 YSGYKVEFSGNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAV 475
 419 HSGYKVEFSGNDITSPRYGKSSPEYONLENGEKYRRAVANTLAWP-----SAV 478
 476 VMCEFLMOSRGITPVLWTNHSKVDFFNMIDSKITQLPLKAYKALQSGASVYAGPRTGG 535
 479 VRCEFLMOSRGITPVLWTNHSKVDFFNMIDSKITQLPLKAYKALQSGASVYAGPRTGG 538
 536 DIIOCTENGSAATYIV--PVSYSOKYRAIRIHASTQSITFTISLDGAPRNOYEPDKTI 593
 539 DIIOCTENGSAATYIV--PVSYSOKYRAIRIHASTQSITFTISLDGAPRNOYEPDKTI 597
 594 NKGTITVNSFNLSFSPFELS--GNMLQIGVTGLSAGDKYIYDKIEFIPVN 644
 598 DKGTITVNSFNLSFSPFELS--GNMLQIGVTGLSAGDKYIYDKIEFIPVN 649

RESULT 3
 C3BB_BACTU STANDARD: PRT: 652 AA.
 ID C3BB_BACTU 006117: 045717:
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidicidal crystal protein cry3ab (insecticidal delta-endotoxin
 DE CryIIIB(b) (Crystaline entomocidal protoxin) (74 kDa crystal
 DE protein).
 GN CRY3AB OR CRYIIIB(b) OR CRYIIIB2.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1428;
 RN SEQUENCE FROM N.A.
 RP STRAIN=EG4961.

RA MEDLINE-93119147; PubMed-1476436;
 RA Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke M.C.,
 RA Johnson T.B.;
 RT "Characterization of two genes encoding Bacillus thuringiensis
 RT insecticidal crystal proteins toxic to Coleoptera species";
 RT Appl. Environ. Microbiol. 58:3921-3927(1992).
 (2)

RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18655 / EG5144;
 RA Donovan W.P., Rupar M.J., Slaney A.C.;
 RT "Bacillus thuringiensis cryIIIC, (b) protein toxic to coleopteran
 RT insects";
 RT Patent number US5378625, 03-JAN-1995.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA. HAS MODERATE LEVEL OF TOXICITY TO
 CC SOUTHERN CORN ROOTWORM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
 CC THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
 CC TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).

CC EMBL: M89794; AAA2334.1: -
 DR EMBL: U31633; AAA74198.1: -
 DR HSSP: P07130: IDIC.
 DR InterPro: IPR001178: Endotoxin.
 DR Pfam: PF00555: endotoxin.1.

Q -> P (IN STRAIN EG5144).
 N -> D (IN STRAIN EG5144).
 I -> V (IN STRAIN EG5144).
 F -> S (IN STRAIN EG5144).
 VYL -> IYF (IN STRAIN EG5144).
 S -> G (IN STRAIN EG5144).
 L -> I (IN STRAIN EG5144).
 K -> T (IN STRAIN EG5144).
 K -> T (IN STRAIN EG5144).
 K -> T (IN STRAIN EG5144).

Query Match 68.7%: Score 2341.5; DB 1: Length 652;
 Best Local Similarity 68.6%: Pred. No. 146-146;
 Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;

1 MNPNNRSEHDTIKTENNENPTNHNVOYPLAETNPPTLEDLNKKEFLRMADNTEALDSS 60
 1 MNPNNRSEHDTIKTENNENPTNHNVOYPLAETNPPTLEDLNKKEFLRMADNTEALDSS 60
 61 TTKDVIOKGISVVDLGIVGPPFGALVSFTYNTPLNTIPSPDPMKAFMEVQALMDOK 119
 61 TTKDVIOKGISVVDLGIVGPPFGALVSFTYNTPLNTIPSPDPMKAFMEVQALMDOK 120
 120 KIDYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSOGRIRELFQAESHFRNS 179
 121 KIDYAKKALAELOGIANNVEDYVSALSSWOKNPVSSRNPHSOGRIRELFQAESHFRNS 180
 181 SMPSFAISGEVLEFLTYAQAANTHLEFLDKDAQYGEEMGEKEDIAEFYKROLKLOET 239
 181 SMPSFAISGEVLEFLTYAQAANTHLEFLDKDAQYGEEMGEKEDIAEFYKROLKLOET 240
 240 TDHCYKWNVGLDKLRGSSYSWNNENRYRREMTLTVDLIALFPYDVALYKREVKTELT 299
 241 TDHCYKWNVGLDKLRGSSYSWNNENRYRREMTLTVDLIALFPYDVALYKREVKTELT 300

QY 300 TRDVLTPDPIGVNNLRGCTGTFESNIENYIRKPHLEFDYLRHQFHTROPQGYGNDSENYW 359
 DB 301 TRDFTDPIFSLNLOEYGPFLSEIENIRKPHLEFDYLRHQFHTROPQGYGNDSENYW 360
 QY 360 SGNVSTPSTSGSNDITSPYGGKSEPVONLEFNGEKYRAVANINLAWP5A-VYSG 418
 DB 361 SGNVSTPSTSGSNDITSPYGGKSEPVONLEFNGEKYRAVANINLAWP5A-VYSG 420
 QY 419 VTKVEFSQVNDQDEASTQYDYSKRNVAVS-MDSIDQLPPTTDEPLEKGYSHQNLVYM 477
 DB 421 VTKVDFEQYDDQKNETSTQYDYSKRNVAVS-MDSIDQLPPTTDEPLEKGYSHQNLVYM 480
 QY 478 CFLMGSRGITPVLTWTHRSVDFPNMDSKRTIQLPLVKAAYKQSGASVAVAGPRTGDI 537
 DB 481 CFLMGSRGITPVLTWTHRSVDFPNMDSKRTIQLPLVKAAYKQSGASVAVAGPRTGDI 540
 QY 538 IQCTE-NGSANTIVYT-PDVSYSQKRYARIRHVASTQITFTLSLDGAPNOYFDTINK 595
 DB 541 LFLKSSNSIAKPKVTLNSAALLQRYRVRIRASTTNLRFVONSNDLVYINKTKMK 600
 QY 596 GDLTYNSFNLSFSTPELFG--NNLQIGVTGLSAGDKVYIDKIEFIV 643
 DB 601 DDLTYOTDPLATNSNMFGSGDKNELLIGAESFVENEKIYIDKIEFIV 650

RESULT 4

ID C3BA_BACTO STANDARD; PRT; 659 AA.
 AC P17969;

DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cry3Ba (Insecticidal delta-endotoxin
 DE CryIIIBa) (Crystalline entomocidal protoxin) (75 kDa crystal
 protein).
 GN CRY3BA OR CRYIIIB(A) OR CRYIIIB.
 OS Bacillus thuringiensis (subsp. tolworthi).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 RX NCBI_TaxId=1442;

RP SEQUENCE FROM N.A.

RC STRAIN=43F;
 RA MEDLINE=90206811; PubMed=2320431;
 RA Sick A., Gaertner F.H., Wong A.;
 "Nucleotide sequence of a coleopteran-active toxin gene from a new
 RT isolate of Bacillus thuringiensis subsp. tolworthi.";
 RL Nucleic Acids Res. 18:1305-1305(1990).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: X17123; CAA34983.1; -;
 DR EMBL: A07234; CAA00645.1; -;
 DR PIR: S10228; S10228.
 DR HSP: P07130; IDLC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 DR Toxin: Sporulation.
 SO SEQUENCE 659 AA; 75159 MW; 5A5B21A8F84160CA CRC64;

Query Match 67.7%; Score 2307.5; DB 1; Length 659;
 Best Local Similarity 68.0%; Pred. No. 2.4e-144;
 Matches 442; Conservative 75; Mismatches 126; Indels 7; Gaps 6;

QY 1 MNPNNSEHDITKTENNEVPNNHVOYPLAEPNPLEDLNKEFLRMTADNNFALSS 60
 DB 9 MNPNNSEHDITKTENNEVPNNHVOYPLAEPNPLEDLNKEFLRMTADNNFALSS 68
 QY 61 TTKDVIQAKISVYDGLGVGPPFGGALVSEYTNFLNTWPS-DPWKAFMEQVETALMDQ 119
 DB 69 TVKDAVGVGISVVGQILGVAVGVPFAGALTSFQSEFLNIMPSPDAPKAFVAVQVEVLIDK 128
 QY 120 KIADYAKNKAELQGLONNVEDYVSAISSQKNNVSSRNHSGRIEELSQAESHFRN 179
 DB 129 KIEEYAKSALAEGLQONNEDYVSAISSQKNNVSSRNHSGRIEELSQAESHFRN 188
 QY 180 SMPFAISGEVYELFTTYAQAANTHLLFLKDAQIYGEEMGEKEDIAEFYRQKLTQY 239
 DB 189 SMPFAISGEVYELFTTYAQAANTHLLFLKDAQIYGEEMGEKEDIAEFYRQKLTQY 248
 QY 240 TDHCYKMYNNVGLDKRGSSYESVNNFRNRRKMTLVLDLALPPLDYVRLYPREVETEL 299
 DB 249 TDHCYKMYNNVGLDKRGSSYESVNNFRNRRKMTLVLDLALPPLDYVRLYPREVETEL 308
 QY 300 TRDVLTPDPIGVNNLRGCTGTFESNIENYIRKPHLEFDYLRHQFHTROPQGYGNDSENYW 359
 DB 309 TRDFTDPIFSLNLOEYGPFLSEIENIRKPHLEFDYLRHQFHTROPQGYGNDSENYW 368
 QY 360 SGNVSTPSTSGSNDITSPYGGKSEPVONLEFNGEKYRAVANINLAWP5A-VYSG 418
 DB 369 SGNVSTPSTSGSNDITSPYGGKSEPVONLEFNGEKYRAVANINLAWP5A-VYSG 428
 QY 419 VTKVEFSQVNDQDEASTQYDYSKRNVAVS-MDSIDQLPPTTDEPLEKGYSHQNLVYM 477
 DB 429 VTKVDFEQYDDQKNETSTQYDYSKRNVAVS-MDSIDQLPPTTDEPLEKGYSHQNLVYM 488
 QY 478 CFLMGSRGITPVLTWTHRSVDFPNMDSKRTIQLPLVKAAYKQSGASVAVAGPRTGDI 537
 DB 489 CFLMGSRGITPVLTWTHRSVDFPNMDSKRTIQLPLVKAAYKQSGASVAVAGPRTGDI 548
 QY 538 IQCTE-NGSANTIVYT-PDVSYSQKRYARIRHVASTQITFTLSLDGAPNOYFDTINK 595
 DB 549 LFLKSSNSIAKPKVTLNSAALLQRYRVRIRASTTNLRFVONSNDLVYINKTKMK 608
 QY 596 GDLTYNSFNLSFSTPELFG--NNLQIGVTGLSAGDKVYIDKIEFIV 643
 DB 609 DDLTYOTDPLATNSNMFGSGDKNELLIGAESFVENEKIYIDKIEFIV 658

RESULT 5

ID C8AA_BACUR STANDARD; PRT; 1157 AA.
 AC Q45704;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry8Aa (Insecticidal delta-endotoxin
 DE CryVIIIa) (Crystalline entomocidal protoxin) (131 kDa crystal
 protein).
 GN CRY8AA OR CRYVIII(A).
 OS Bacillus thuringiensis (subsp. kumamotoensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 RX NCBI_TaxId=132267;

RP SEQUENCE FROM N.A.

RC STRAIN=NRRL B-18746 / PS50C;
 RA Payne J.M., Sick A.J., Fonceirada L.;
 RT "Novel coleopteran-active Bacillus thuringiensis isolate and a novel
 RT gene encoding a coleopteran-active toxin.";
 RL Patent number EP0498537, 12-AUG-1992.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.

CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.

CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

DR EMBL: U04364; AAA21117.1; -

DR HSSP: P07130; IDLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

KW Toxin; Sporulation.

SO SEQUENCE 1157 AA; 131009 MW; 687B5C49DE93683B CRC64;

Query Match 36.4%; Score 1240; DB 1; Length 1157;
Best Local Similarity 40.2%; Pred. No. 8.7e-74; Mismatches 231; Indels 62; Gaps 17;
Matches 275; Conservative 116;

1 MNPNNREHDTITKTENNEVPTNHVQPLAETPNPLEDINTYKEFLMTADNTEALDSS 60
1 MSPNNONEYEIIDTPTSTVSSDSNRKPFANPEPTDANNYKDYLMKSGENPELEGNP 60

61 TT--KDVIGKISVVDLLGVVGFPGALVSFTYNTLTPMPSE--DPMKAFMEGYEA 115
61 ETFTSSSTIGTIGIYVRIIGALGVFPASQIASFTYVQOLMPSKVDITMGEIMEVEE 120

116 LMDDKINDYKKNKALAELOGLONNVEDYVYALSSWOKNPSRNPBSQGRIRLEFSQAE 175
121 LVDDKIEKYKDAELKLGKGNALDYQOSLEDMENRNDAR--TRSVYNGFIIDL 177

176 HFRNSMPSFASISGEVLEFLTYTAOANTHLFLKDAQIYGEEMGYEKEDIAPFKROLK 235
178 NFVSSISFASVSGHEVLLAVYAOAVMLHLRLDASIFGEHGFPTGGEISRFYNROVOL 237

236 TOEETHDCVKNYVNGDLKRGSSSESVNPNRYRREMTLVLDIALPFLYDVALYKREV 295
238 TAEVSDVCVKNYKIGDLKGTSTKSLNHLQFRREMTLVLDVALPNDYTHMYET 297

296 KTELRLDVLTPDIY-GVNNLGRY-----GTFESNIE-NYIRKPHFLDYLRHQEHR 345
298 TAOITRQVYTPPIAFNIVTSTGFCNPMSTHSGILFEVENNVIRPHFLDILSSVEINTS 357

346 FQPGYVNDSEF-NVWSGMYVSTSPISGNDITTSPEYGNKSE-----P 388
358 RGGITLNDAYINWSGHTLKYRTTADSTVYTAN-YGRITSEKNSFALDIEDRDIFEINST 416

389 VONLEFNKEKYRAVANNNLAVMPASVYSGVTKVEFSQYNDQTD--EASTQYVSKRWVG 446
417 VANLANIYQKAGVPGS-----WFRMVKRGSTTAYLSTKTHALQCTQVYESS----- 467

447 AVMSIDQLPETDEPLEKGYSHQNLVYM--CELMQGR--GTIPVLTTHRSVDFN 502
468 -----DEPLDRT-VVAESYSHRLSHTSFSGNSAAYSGFVFWTTHSADLNN 519

503 MDSKKTITQLPLVAKYKQASQSVAGPRFGGDIIOCTENGSATITVTDVYSOKYR 562
530 TYSKTIQIIPAVKMDMLYLGSSVQVGGPFGDILKTKTNPISILCTFVAVYNGSLQKR 579

563 ARIHASTSQTFTSLDCAPENOYFPDKINKGDTLITNSENFLASFTPEEL--SGNUL 620
580 VAIKRASTIDREFITLTL-GDTIEKRNFRKMTDMNGASLTYETPKFASFTIDQFRETQKI 638

621 QIGVTLGSLAGRVYIDKIEFIPVN 644
639 LTSMGDESSGDEVYIDRIEFIPVD 662

RESULT 6

CC8A_BACUR STANDARD; PRT; 1169 AA.

ID CC8A_BACUR

AC 045705;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Peptidicidal crystal protein cry8Ba (insecticidal delta-endotoxin

DE CryIIIB(a)) (Crystalline entomocidal protoxin) (134 kDa crystal

DE protein)

GN CRIBBA OR CRYIIIB(a) OR 50C(B).

OS Bacillus thuringiensis (subsp. kumamotoensis).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID-132267;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NRRL B-16746 / PS50C;

RA Michaels T.E., Fencera U., Narva K.E.,

RT "Process for controlling scarab pests with Bacillus thuringiensis

RT isolates."

RL Patent number WO9315206, 05-AUG-1993.

CC - FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABEID BEETLES.

CC - DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC - MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC - SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

DR EMBL: U04365; AAA21118.1; -

DR HSSP: P07130; IDLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

KW Toxin; Sporulation.

SO SEQUENCE 1169 AA; 133543 MW; 22EECF5BD699909 CRC64;

Query Match 34.9%; Score 1187; DB 1; Length 1169;
Best Local Similarity 38.8%; Pred. No. 2.7e-70; Mismatches 260; Conservative 141; Mismatches 231; Indels 38; Gaps 22;

1 MNPNNREHDTITKTENNEVPTNHVQPLAETPNPLEDINTYKEFLMTADNTEALDSS 60
1 MSPNNONEYEIIDTPTSTVSSDSNRKPFANPEPTDANNYKDYLMKSGVSETPGSP 60

61 -----TTKDVIGKISVVDLLGVVGFPGALVSFTYNTLTPMPSE--EDPMKAFMEGYEA 114
61 EVFLSEGDANKAALDIYKGLTIGVFPVGPPIYSLVQLDILMPSKQSGMEIFMEGYEA 120

115 ALMDQKADYAKKALAELOGLONNVEDYVYALSSWOKNPSRNPBSQGRIRLEFSQAE 174
121 ELINOKIAEYARNAKALSELGLGNVQLYLTALKEWENENGR--ALDVRNREIIDL 177

175 SHFRNSMPSFASISGEVLEFLTYTAOANTHLFLKDAQIYGEEMGYEKEDIAPFKROLK 234
178 SLFTQYMPSEFVNTFEPEFLTYTAOANTHLFLKDAQIYGEEMGYEKEDIAPFKROLK 237

235 LTOEETHDCVKNYVNGDLKRGSSSESVNPNRYRREMTLVLDIALPFLYDVALYKREV 294
238 LTAESDVCVKNYKIGDLKGTSTKSLNHLQFRREMTLVLDVALPNDYTHMYET 297

296 KTELRLDVLTPDIY-GVNNLGRY-----GTFESNIE-NYIRKPHFLDYLRHQEHR 348
298 TTAQITRQVYTPPIAFNIVTSTGFCNPMSTHSGILFEVENNVIRPHFLDILSSVEINTS 356

QY 349 GYVNDSPNWSNGVSTRPSIGSNDITSPFYGNKSSSEPVONLENGEKYRAVANTLU 408
 Db 357 SFTSDRYMRWAGHQISYK-HIGTSFTQMYGTQNLQSTSNFPTNNDIKTISNNAV 415
 QY 409 ---AVMPSAVYS--GVYKVEFSQYNDOTDEASTQY-DSKRVYGAWSIDQLPPTTD 462
 Db 416 LLDIVYGYTYTTPGMEPEEFVNOJLNNRKLTYKPAKSDIIDRTNRESELEPPTSG 475
 QY 463 EPLEKGYSHOLNYMCFMLOGSNGT-IPVLWTMHSVDFENMIDSKKITOLYVAYKLO 521
 Db 476 QPNVESYSHRLGHI-TEIVSSSTVYVPVPSMHRASADLTNTYKSGEITOLPGKSSITG 534
 QY 522 SGASVYAGPRFTGDIIOCTEN-GSAATYVTPDVYSOKYRARIHYAS--TSQIT-FTL 577
 Db 535 RMTYIKRGRTGGLVALTLDRIGSCFQMIPPE--SQRFRIIRYASNETSYSLYGL 591
 QY 578 SLUGA-PFNQYFDTKINKGDTLYNSFNLASPTPEFL-SCNNQIOGVTLGASGDKYI 635
 Db 592 NQSGTLKFNQYTSNK--NEND-LTYNDFYIEYPRYISVYASSNTIOLSIGIQTNTMLFI 648
 QY 636 -DKIEFTPVN 644
 Db 649 LDRIEFTPVN 658

RESULT 7
 CLIB_BACTE STANDARD: PRT: 719 AA.
 AC 045709;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin
 DE CryII(b) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
 CN CRYIIB OR CRYIIB(b) OR CRYV OR CRYV465.
 OS Bacillus thuringiensis (subsp. entomocidus).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1436;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BP465;
 RX MEDLINE=95314293; PubMed=7793960;
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.I.;
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus
 thuringiensis and cloning of cryV-type genes from Bacillus
 thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
 RT entomocidus." Microbiol. 61:2402-2407(1995).
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
 CC ACTIVE ON PLUTELLA XYLOSTELLA BUT NOT ON BOMBYX MORI.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
 CC or send an email to license@isb-sdb.ch).
 CC EMBL: U07642; AAA82114.1; --
 DR HSSP: P02965; ICIT.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SO SEQUENCE 719 AA; 81295 MW; E8210ABEA97688E CRC64;

Query Match 34.6%; Score 1178; DB 1; Length 719;
 Best Local Similarity 38.6%; Pred. No. 5,3e-70;
 Matches 256; Conservative 132; Mismatches 234; Indels 42; Gaps 15;

QY 1 MNPNNRSEHDTIKTTEN-NEVPNNHYQPLATPNT---LEDLWYKFEKLRATNNTA 56
 Db 1 MKLKNPKKHOSLSNAKVDKIATDSLK-----NETDIEKNNMNEYLRN--SEHS 50
 QY 57 LBSSTTKDVIQKISVYGDLLGVYGFPGALVSEYTFNLTNP-SDPWKAFMEQVEA 115
 Db 51 IDPFVSASTIQTIGIAGKITGLTGVFAGQIASLYSFLIGLWKKGSCQMEIFENHAE 110
 QY 116 LMDOKIADYAKNKALELOGLONNVNDYISALSSQKNKPNVSRNPHSGRIRELSQAES 175
 Db 111 IINQKILTYTARKNALSGLDGLDALVYHESLESWEV---RNNRARSVYKNOYIALEL 167
 QY 176 HFRNSMPSFASISGEVLEFTTYAQAANTHLFLKNOAYIGEEMGEKEDIAEFKROLK 235
 Db 168 MFYQKLPSPFVSGEEVPLPIYAQAANHLHLLRDSIFGKEMGLSASEISTFYNRQVER 227
 QY 236 TOEYTHCYKWTNVCGLDKLRGSSYSWVNFNRYREMTLVLDLITALEPLTVRLYREV 295
 Db 228 TRDYSDHCIKWNTGILNNLRGTNAKSWRYNQFRKDTLAVLDLVALPSPYDVLVPIKT 287
 QY 296 KTELEFQDVLTDPIVGVNNGYGT-----PSNIE-NYIKRPHFDYLRHIOFH-- 343
 Db 288 TSQITREYVTDALGVYHPQAFASITWTNNNAPSFALEAAVHSPLDLFEKVTYSL 347
 QY 344 -TRPQGYGNDSPFVYSGNVSSTRPSIGSNDITSPFYGNKSSSEPVONLENGEKYRA 402
 Db 348 LSWMSWTOY---MMWGGHRLSPRGALNTSFG-SWTSTINPV-TIQFTSRDYRT 401
 QY 403 VANTMLAVPWSAVYSGVYKVESQYNDOTDEASTQYD-SKRANGAVSWSIDQLPPTT 461
 Db 402 ESTAGLNFLETPVGVGPRVDMKEPPLPIASNFYLLGAYAGTQLOQOSEMELPETT 461
 QY 462 DEPLEKGYSHOLNYMCFMLOGSNGTIPVLWTMHSVDFENMIDSKKITOLYVAYKLO 521
 Db 462 GQPNVESYSHRLSH--GLISAHYKALVYSWTHRSADRTNTPNSITPIPLKKNLS 519
 QY 522 SGASVYAGPRFTGDIIOCTENGSAATYVTPDVYSOKYRARIHYASTQITFTSLDG 581
 Db 520 SGAAYVRRPFGGLDIRNTGTGFDIRVNNIPFAQRYVRIRYASTDLOFHNSING 579
 QY 582 APFNQYFDTKINKGDTLYNSFNLASPTPEFLS--NNLQGVYGLSGDKVYIDKIE 639
 Db 580 KAINGNFSATMNGEDLDYKTFITFTTFFSFDVQSTFTIGAMNFSNGEYTDRIE 639
 QY 640 FIVP 643
 Db 640 FIVP 643

RESULT 8
 CLIB_BACTU STANDARD: PRT: 719 AA.
 AC 09XDL1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pesticidal crystal protein cryIId (insecticidal delta-endotoxin
 DE CryIId) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
 CN CRYIID OR CRYIID(b) OR NRCRYV.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1426;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BR30;
 RX MEDLINE=20374042; PubMed=10919402;
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;
 RT "Cloning of a new Bacillus thuringiensis cryIId-type crystal protein

RT gene.;

CC Curr. Microbiol. 41:65-69(2000).

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE. ACTIVE ON PLUTELLA

CC XYLOSTELLA AND ON BOMBIX MORI.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC C-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>

CC or send an email to license@isb-sdb.ch).

CC -----

DR EMBL: AF047579; AAD44366.1; -

DR HSP: P02965; 1C1Y

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00355; endotoxin; 1.

KW Toxin; Sporulation.

SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 34.5%; Score 1176.5; DB 1; Length 719;

Best Local Similarity 40.4%; Pred. No. 6.7e-70;

Matches 256; Conservative 114; Mismatches 232; Indels 31; Gaps 12;

QY 28 PLAEPTLEEDLYKFEKRLMTADNTEALDSTTKDYIKGISVVDLLGVGFPFGA 87

DB 25 PLEHNTMELONSHEEDCKMKESEVEPEFVSST--IGTGIGIAKIGLGNLGPAGQ 81

QY 88 LVSTYTNPLNTIP-SEDPKAKMEQVEALMDQIADYAKNAKLAELGLONNEDVSA 146

DB 82 VASLYSFLIGLWPKGSQWEIEMEHEVELNOKISTYARKKALADKGLADALANVHES 141

QY 147 LSSQKPNVSSRNPHSOGRIELFSQAESHRNPSFAISGVEVLFLLTYAQAANTHLP 206

DB 142 LESHTEN---KNNTRVSVYVKNQIADLELMVQKLPFASVSGEEVPLPIYAQAANHL 198

QY 207 LKDAQIYGEEMGYEKEDIAEFYRQKLTQDEYDHCWKYNGVLDKRGSSYSWYFN 266

DB 199 LLRDAISFGKEMGLSESEISPFYNNROSSQDCEYDCEWYNTGLNRLGTNAESWVYN 258

QY 267 KYRREMTLVLDLALPPLVVRVRLXPKVEKELRDVLTDPVGNMLRGGT----- 320

DB 259 QFRDMTLMVLDLALPFSYDTRMTPIPTSAQLTREVYTDALGIVHNPASASTTWYNN 318

QY 321 ---SNIE-NYIRKPHLFYDLHRIQF---TRQPGYVYNDGFYWSGVNSTRPSISN 373

DB 319 APSSTEDIAAVRNPHLDLEQVYIYSLSRWSNTQY---MMNGGSHKLEFR-TIGGT 373

QY 374 DIISPFYGNKSSPEVQVLENGEYVRAVANTLAWPSAVSYGVTVES-QYNQDQD 432

DB 374 LNTSTQSTNTSINPV-FLPPTSBDVYRTESLAGLNTLPVNGVPRVDMHMFVHPPI 432

QY 433 EASTQYVSKRNQVAVWDSIDOLPEPTDEPLEKGYSHQNVYVCFMQSSRGTPYLT 492

DB 433 ASDNYYVGYAGIGTOLDSENEPPEPTTGPQNTSYSHRSLH--GLISASHKALYVS 490

QY 493 WTKASVDFNMIDSKKTIQPLVAKYKLSQASVAVAGPFGGDIIGCTENGSAATYVT 552

DB 491 WTHRSADRNRTINSDSITQIPLVAKAFNLPSCASVAVRGEGFGDILQRTNGTEGDIYVN 550

QY 553 PDVYSQKRAIRIHASVQITFLSLDGAFFNQYFDKTIKNGDGLLYNSNLAFFSTP 612

DB 551 INPPAQRRLIRIRYASTTNEEHTSINKALINQNSFATMNRGDLDKARIVYGFITP 610

QY 613 FELSG--NNLQIGVTGLSAGDKVYIDKIEFIV 643

DB 611 FFSNASTFTTIGANNFSLNGEVYIDRIEYV 643

RESULT 9

CC C7AB_BACUK STANDARD; PRT; 1138 AA.

AC 045708;

DR 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DR 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cry7ab (insecticidal delta-endotoxin

DE cry7ab(b) (crystalline entomocidal protoxin) (130 kDa crystal

DE protein).

GN CRY7AB OR CRYVIA(B).

OS Bacillus thuringiensis (subsp. kumamotoensis).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OK NCBI_TaxID=133267;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HD867;

RA Payne J.M., Fu J.M.;

RT Coleopteran-active toxins.*;

RT coleopteran-active toxins.*;

RL Patent number US5286486, 15-FEB-1994.

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF COLEOPTERA.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC C-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>

CC or send an email to license@isb-sdb.ch).

CC -----

DR EMBL: U04368; AAA21121.1; -

DR HSP: P07130; 1DLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00355; endotoxin; 1.

KW Toxin; Sporulation.

SQ SEQUENCE 1138 AA; 129658 MW; E12DC80C0A56DIDA CRC64;

Query Match 34.5%; Score 1174.5; DB 1; Length 1138;

Best Local Similarity 38.3%; Pred. No. 1.7e-69;

Matches 258; Conservative 114; Mismatches 235; Indels 67; Gaps 18;

QY 1 MNPNNSEHDTITTEENVEPTNHYQPIAETNPTELELYKELMTADNTEALDSS 60

DB 1 MNLNLTAGVE---DSNRTLNNSLNPTQKALSPKNNYDPLSITERQPEALAG 55

QY 61 TTKVDYQKISVVDLLGVGFPFGALVSFYTNPLNTIP-SEDPKAKMEQVEALMDQ 119

DB 56 NT-AINTVAVSYVCATLSALGVPGASFTNFKITGLMPHDKNTMDEPTEVEFLIQ 113

QY 120 KIADYAKNAKLAELGLONNVEDVSAISSMOKNPVSSRNPHSOGRIELFSQAESHRN 179

DB 114 KIEQYAKNAKLAELGEGNNTIYQOALDEMNNP---DDPATTVYIDRFLDALFES 170

QY 180 SMPFASIGVEVLFLLTYAQAANTHFLKDAQIYGEEMGYEKEDIAEFYRQKLTQY 239

DB 171 YMFSEFVAGEIPLLLTYAQAANHLALDLSDYLGKMEFTQNNLENNRKKHISEY 230

QY 240 TDHCVKVNVGDLKRGSSVSVNFRYRREMLTVLDLALPPLVDRVLPREVTEL 299

DB 231 SNHCVKWNTNSGLSRNGSTIYQWNTNFRFREMILMVDLAAVFPYIDPDMYSMETSTOL 290

QY 300 TRDVLTDPI-VGVNMLRGYGTTFSENEN-YIRKPHLFYDLHRIQFHT-----RFQPG 349

```

Db 291 TREYVTPDISLISN-DGIPSPSOMENTAIRPHLDVYDELYTSKKAESHEIQPD 349
Qy 350 YGNDSPNMGVNSGNYSTRPSIGSNDITSPFYGNKSEPVQN--LEFNGEKYRAVANTN 407
Db 350 LF-----YSAHVSFKSEQSN-LTTGTIGY-KTSGYISSGAVSRGDIYRTLAAPS 401
Qy 408 LAVPMSAVYSGVTKEVSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEK 467
Db 402 VVVVPPYQNVGEQVEFYGKGVHVGNDKVD-----LTVDSIDQLPPD--GEPIHE 452
Qy 468 GYSHOLNVYVCFLMG--SRGITPVLTWTHKSVDFPNMIDSKKITQLPLVAKYKLSQSA 524
Db 453 KYTHRLCHATAISKSTPDYDNATIPFSWTHRSAEYNNRIYPNKIKIPAVKMKLGDS 512
Qy 525 SVVAGPRTGGDIIOCTENGSAATVYTPDVYSQKRYARIHYASTQSITFLSLDCAFP 584
Db 513 TVVKGPGFTGDLVKGNSNGYIDIKATVNSPLSQYRVRARVAVN-----SGOF 563
Qy 585 NOYFEDK-----TINKGDTLYTNSFNLASFSPFELSNGN--LOIGVGTLSAG 630
Db 564 NVYINDKITLQRRKQWVETIGEGKDLTGSGFYIEYSTTIOPDPKHPKITLHLSDLSNN 623
Qy 631 DKYIDKIEPIPN 644
Db 624 SSFYVDSEIPIVD 637

RESULT 10
C7AB_BACUA STANDARD: PRT: 1138 AA.
AC 045707:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pesticidal crystal protein cry7Ab (insecticidal delta-endotoxin
DE protein) (crystalline entomocidal protoxin) (130 kDa crystal
GN CRY7AB OR CRYVIIA(B).
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_Taxid=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HD511;
RT Payne J.M., Fu J.M.:
RT "Coleopteran-active toxins";
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U04367; AAA21120.1; -.
CC HSSP: P07130; 1DLC.
CC InterPro: IPR001178; Endotoxin.
CC Pfam: PF00555; endotoxin; 1.
CC Toxin: Sporulation.
CC SEQUENCE 1138 AA; 129778 MW; 01DF072C074CE88 CRC64;

```

```

Query Match 34.0%; Score 1159.5; DB 1; Length 1138;
Best Local Similarity 38.2%; Pred. No. 1,7e-68;
Matches 254; Conservative 119; Mismatches 243; Indels 49; Gaps 17;

Qy 1 MNPNNSEDDTJKTENNENPETHVQYPLAETPNLTDLVNYKEFLRYTAONNTAALSS 60
Db 1 MNLNLGGE-----DSNLTNLSNLTPTQKALSLKLNMYODLTSTEDEQEPALASG 55
Qy 61 TTKDVIQKISVYDGLGVGPPFGCALVSEYTNFLNTIMP--SEDPKAFMEQVEALMDQ 119
Db 56 NT--AINTVSVTGAATLALGVPGASFTTNFLYKLTGGLMHPNKNIMDEFTVEETLEQ 113
Qy 120 KIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNHSGRITRELSQAESEHFN 179
Db 114 KIEQYARKKALAELEGLONNLTITQALDMLNPN--DDPATYTRVLDRIIDLALFES 170
Qy 180 SMPFAISGEVYELFTTYAAQANTHLFLKDAQIYGEEMGEKEDIDAEFYRQLKLOEY 239
Db 171 YMPSEFRVAGEIPIPLTYAAQANLHLALRDLSTLGDKNFTQNNIENYRQKKHISEY 230
Qy 240 TDCYKATNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPELVYDLRYPREVTEEL 299
Db 231 SMHCYKMYNSGLSRNGSTYEQMINYRFRREMLLVLDIAAVPIYDPRMYSMETSTOL 290
Qy 300 TRDVLTPDI-VGVNVLRGYGTFSNEN-YIRKPHLDYLRIOFHT-----RQPG 349
Db 291 TREYVTPDISLISN-PDIPSPSOMENTAIRPHLDVYDELYTSKKAESHEIQPD 349
Qy 350 YGNDSPNMGVNSGNYSTRPSIGSNDITSPFYGNKSEPVQN--LEFNGEKYRAVANTN 407
Db 350 LF-----YMCVHKVSEFKSSQSN-LYTTGIGY-KTSGYISSGAVSRGDIYRTLAAPS 401
Qy 408 LAVPMSAVYSGVTKEVSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEK 467
Db 402 VVVVPPYQNVGEQVEFYGKGVHVGNDKVD-----LTVDSIDQLPPD--GEPIHE 452
Qy 468 GYSHOLNVYVCFLMG--SRGITPVLTWTHKSVDFPNMIDSKKITQLPLVAKYKLSQSA 524
Db 453 KYTHRLCHATAISKSTPDYDNATIPFSWTHRSAEYNNRIYPNKIKIPAVKMKLGDS 512
Qy 525 SVVAGPRTGGDIIOCTENGSAATVYTPDVYSQKRYARIHYASTQSITFLSLDCAFP 584
Db 513 TVVKGPGFTGDLVKGNSNGYIDIKATVNSPLSQYRVRARVAVN-----SGOF 563
Qy 585 NOYFEDK-----TINKGDTLYTNSFNLASFSPFELSNGN--LOIGVGTLSAG 630
Db 564 NVYINDKITLQRRKQWVETIGEGKDLTGSGFYIEYSTTIOPDPKHPKITLHLSDLSNN 623
Qy 631 DKYIDKIEPIPN 644
Db 624 SSFYVDSEIPIVD 637

RESULT 11
C1BB_BACTU STANDARD: PRT: 1229 AA.
AC 045739:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIb (insecticidal delta-endotoxin
DE protein) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN CRYIIB OR CRYIB(B) OR CRYETS.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_Taxid=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BG5847 / NRRL B-21110;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.:
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects";
RL Patent number US5322687, 21-JUN-1994.

```

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARAE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREPLATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L32020; AAA22344.1; -
 DR HSSP: P02965; ICIT.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1239 AA: 139769 MW: 140949DB675C3269 CRC64;

Query Match 34.0%; Score 1156.5; DB 1; Length 1239;
 Best Local Similarity 37.9%; Pred. No. 3e-68;
 Matches 250; Conservative 117; Mismatches 254; Indels 39; Gaps 14;

QY 1 MNPNNSEHDITKTENNEVPTNHVQPLAETPNFLE---DLNKEFLMRTADNTEAL 57
 DB 1 MTSNRKNEHEIT-----NALSIPTVSNPSTQNLSPDRIEDSLCVAEENNIDPF 50
 QY 58 DSSTKDVIOGISVYDGLGVGPPGALVSYFTNFTLTPS-EDPKAFMEQVEAL 116
 DB 51 VSAST---VQGINIAGRIIGLVGVPAGOLASFISVLGELMPSRDRPWEIYLEHEDL 107
 QY 117 MDQRIADYAKKNAELQGLONNVEDYVALSSMOKNPVSSRNPHSGGRIRLEPSQAESH 176
 DB 108 IRQOYTEMTRTAIRLEGGRYSYQALFTWLDNRNDR---SRSIILEYVLELD 164
 QY 177 FRNSMPFAISGEVLEFLTYAQAANTHLFLLKAOIYGEEMGEKEDIAEFKROKLT 236
 DB 165 ITTALPIRINEEVPPLMVAQAANLHLRLDASLGSEMGMASSDVNOYIOEORIT 224
 QY 237 OEYTDHCWKYVNGDLKRGSSYEWNFNRYRREMTLVLDLALFPLVDRLYPREK 296
 DB 225 EYSNHCQWYNTGLNLRGTAESWLRYNQFRDLTGLVDLVALFPSTRTYPIINTS 284
 QY 297 TELTRDVLTPDIVGVNLRGCTT-----FSNIENYI-KRPHLFDYLRIQFTRF 346
 DB 285 AQLTREITVDIGRTNAPSGFASINWFNNAPSPSAIEALFRPHILDEPEOULTISA- 343
 QY 347 QPGYVNDSPFYMSGNVYSTRPSIGSNDLITSPFYGNKSSPEYONLEFNEKYRAVANT 406
 DB 344 SSRWSSTQHMNTWGHRLNFRPIGTLNTSTOGLTNNTSINPV-TLOFTSDYRTRESNA 402
 QY 407 MLAVPSAVYSGVTKVEFSQYNDOT-DEASTQYTDK-RNNGAVSWDSIQOLPETTDER 464
 DB 403 GTNIIFFTYPVNGVPAARENFINPQNIYERATYISOPVQVGIOLFSETELEPETTERP 462
 QY 465 LEKQSHQNLVYMCFLMGSGRGTIPVLFWTHKSYDEFNMDSKITDLPVAKAKLOSGA 524
 DB 463 NYESSHSRHSI--GLIIGNTLRADVSWTHRSADRITTPANITQIPLKALNLSGV 520
 QY 525 SYVASPREFTGDIQCTENGSAATVYTPDVYSOKYRARIHYASTQOITFTLLSDGAPF 584
 DB 521 TVVGSGPCTGDIILRTNMGTCFGRILNINIVPLSQRVVRIRVASTMDIOLFFRTITV 580
 QY 585 NQYEDKTIKGDITLTYSFNLAISTPEL--SGNNQIGVITGASGDKYIKXIEIP 642
 DB 581 NIGNSRTMNRGNDLEYSFRTAGSTPEPNFLNASTFTLLGAQSF--NQEYIDRVERVP 639

RESULT 12
 CIBC_BACTM STANDARD: PRT: 1233 AA.

ID CIBC_BACTM
 AC 045774;
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIbC (insecticidal delta-endotoxin
 DE CRYIbC(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN CRYIbC OR CRYIbC(c) OR CRYIbC.
 OS Bacillus thuringiensis (subsp. morrisoni).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1441;
 OX (1)
 RP SEQUENCE FROM N.A.
 RA Bishop A.H., Bone E.J., Ellar D.J.;
 RT Cloning of novel Bacillus thuringiensis delta-endotoxin.";
 RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREPLATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z46442; CA86568.1; -
 DR HSSP: P02965; ICIT.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1233 AA: 140451 MW: 7318382413529F21 CRC64;

Query Match 34.0%; Score 1156.5; DB 1; Length 1233;
 Best Local Similarity 37.9%; Pred. No. 3e-68;
 Matches 250; Conservative 117; Mismatches 254; Indels 39; Gaps 14;

QY 1 MNPNNSEHDITKTENNEVPTNHVQPLAETPNFLE---DLNKEFLMRTADNTEAL 57
 DB 1 MTSNRKNEHEIT-----NALSIPTVSNPSTQNLSPDRIEDSLCVAEENNIDPF 50
 QY 58 DSSTKDVIOGISVYDGLGVGPPGALVSYFTNFTLTPS-EDPKAFMEQVEAL 116
 DB 51 VSAST---VQGINIAGRIIGLVGVPAGOLASFISVLGELMPSRDRPWEIYLEHEDL 107
 QY 117 MDQRIADYAKKNAELQGLONNVEDYVALSSMOKNPVSSRNPHSGGRIRLEPSQAESH 176
 DB 108 IRQOYTEMTRTAIRLEGGRYSYQALFTWLDNRNDR---SRSIILEYVLELD 164
 QY 177 FRNSMPFAISGEVLEFLTYAQAANTHLFLLKAOIYGEEMGEKEDIAEFKROKLT 236
 DB 165 ITTALPIRINEEVPPLMVAQAANLHLRLDASLGSEMGMASSDVNOYIOEORIT 224
 QY 237 OEYTDHCWKYVNGDLKRGSSYEWNFNRYRREMTLVLDLALFPLVDRLYPREK 296
 DB 225 EYSNHCQWYNTGLNLRGTAESWLRYNQFRDLTGLVDLVALFPSTRTYPIINTS 284
 QY 297 TELTRDVLTPDIVGVNLRGCTT-----FSNIENYI-KRPHLFDYLRIQFTRF 346
 DB 285 AQLTREITVDIGRTNAPSGFASINWFNNAPSPSAIEALFRPHILDEPEOULTISA- 343
 QY 347 QPGYVNDSPFYMSGNVYSTRPSIGSNDLITSPFYGNKSSPEYONLEFNEKYRAVANT 406
 DB 344 SSRWSSTQHMNTWGHRLNFRPIGTLNTSTOGLTNNTSINPV-TLOFTSDYRTRESNA 402

QY 407 NLAWSAVSYGVTKVEFSQYNDOT--DEASTQFYDSK--RNVGAVSWDSIDOLPPEITDDEP 464
 Db 403 GTNILEFTPVNGVPMARFNINQNIYERATITSPYQGVGIGLFDSETELEPETERP 462
 QY 465 LEKYSQHLNVMCMFLMOGSRGTPVLVTHKSVDFPNMIDSKKITQPLVAVAKLOSGA 524
 Db 463 NYESYSHRLSHI--GLTIGCTLRAPYVSWHRSADRTNIGPRITQIPLVAKMLNLSGV 520
 QY 525 SVVAGPFRGTGDIIOCTENGSAATVYTPVYSOKYRARIHAYASTQTFLLSDGAPF 584
 Db 521 TVVGGPFGTGDILRRNTCTGPDILNINVPUSQNTKRVINASTTDLQFTFRINGTIV 580
 QY 585 NQYFEDTKIKGDTLYNNSFNLFASFSTPEL--SGNNLQICVYGLSAGDKVYIDKIEFIP 642
 Db 581 NIGNSFTNMRGNLERSFRAGSTFPENFLMAQSTFLGAQSPS--NQEYIDVNEVEVP 639

RESULT 13

CITA_BACTK

ID CITA_BACTK STANDARD; PRT: 719 AA.

AC Q45752; Q45750; Q45751; Q45756; P71092;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cyIIa (insecticidal delta-endotoxin
 DE CryII(a)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
 GN CRYIIA OR CRYII(A) OR CRYV OR CRYVI OR CGCRV.
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=29339;
 RN NCB1

SEQUENCE FROM N.A.

STRAIN-D51R732;

MEDLINE-93298009; PubMed-8517758;

RA Gieve A.P., Williams R., Hedges R.J.;

RT Screening by polymerase chain reaction of Bacillus thuringiensis

RT serotypes for the presence of cryV-like insecticidal protein genes and

RT characterization of a cryV gene cloned from B. thuringiensis subsp.

RT kurstaki.".

RL Appl. Environ. Microbiol. 59:1683-1687(1993).

RN [2]

RP SEQUENCE FROM N.A.

STRAIN-JHC4835;

RC MEDLINE-92269582; PubMed-1588820;

RA Tallor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;

RT Identification and characterization of a novel Bacillus thuringiensis

RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."

RL Mol. Microbiol. 6:1211-1217(1992).

RN [3]

RP SEQUENCE FROM N.A.

STRAIN-HD-1;

RC MEDLINE-95314293; PubMed-7793960;

RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;

RT Distribution of cryV-type insecticidal protein genes in Bacillus

RT thuringiensis and cloning of cryV-type genes from Bacillus

RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.

RT entomocidus."

RL Appl. Environ. Microbiol. 61:2402-2407(1995).

RN [4]

RP SEQUENCE FROM N.A.

STRAIN-AB88;

RC MEDLINE-96178985; PubMed-8606196;

RA Kostelchka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,

RA Craig J.A., Kozel M.G., Estruch J.J.;

RT Cloning of a cryV-type insecticidal protein gene from Bacillus

RT thuringiensis: the cryV-encoded protein is expressed early in

RT stationary phase."

RL J. Bacteriol. 178:2141-2144(1996).

RN [5]

RP SEQUENCE FROM N.A.

STRAIN-61;

RC Selvendandiyar A., Bhatnagar R.K.;

RT "Isolation, cloning and expression of cryV gene."
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF CERTAIN COLEOPTERAN AND LEPIDOPTERAN SPECIES.
 CC ACTIVE ON PLUTELLA XYLOSTELLA AND BOMBYX MORI.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENOTOXIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M86544; AAA22354.1; -
 DR EMBL: X62821; CAA44633.1; -
 DR EMBL: I36338; AAC36999.1; -
 DR EMBL: I49391; AAB00958.1; -
 DR EMBL: Y08920; CAA70124.1; -
 DR HSSP: P02965; ICTY.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 FT VARIANT 159 159 K -> R (IN STRAIN 61).
 FT VARIANT 233 233 D -> Y (IN STRAIN JHC4835 AND HD-1).
 FT VARIANT 443 443 A -> V (IN STRAIN AB88).
 FT VARIANT 711 712 KO -> NE (IN STRAIN HD-1 AND 61).
 SQ SEQUENCE 719 AA; 81216 MW; 3627E3A6C25DAFE5 CRC64;

Query Match 33.9%; Score 1156; DB 1; Length 719;
 Best Local Similarity 38.0%; Pred. No. 1.5e-68;
 Matches 252; Conservative 132; Mismatches 238; Indels 42; Gaps 15;

QY 1 MNPNRSEHDITKTEEN--NEVPTNVOYPLAEITNPT---LEDNLYKEFLMRTADNTEA 56
 Db 1 MLKMDKHOSFSSNAKYDKISTDSLK-----NEVDIELQNNHEDCKMSYEVEVER 53
 QY 57 LDSSTTKVDYQKISVVDLLGVVGFPGALVFFYNFLMTIWP--SEDMKAFMBOVER 115
 Db 54 FVSAST---IQGIDIAKIIIGTIGVPPAGVAYLTFILGELPKKKNMWFMEHVEE 110
 QY 116 LMDQKIADYAKNKALAEIQGLQNNVEDYVSLSSWQNPVSSRNPHSQGRIRLFSCAQS 175
 Db 111 IINOKISTYARKKALTDLKGLDALAVYHDSLESWGN---RNNTARSYVKQYIALEL 167
 QY 176 HERNSPFAISGYEVLEFTYYAQAANTHLFLKDAQIYGEENEKEDIAEYKQQL 235
 Db 168 MFVQKLPFAVSGEVEPLPPIYAQAAMHLHLMDASIFKEGELSSSESTFFNQOVER 227
 QY 236 TOETIDHCYKVVYNGDLKRGSSYESVWVNFRRYREMTLVLDLIALFLPYDRLPKFV 295
 Db 228 AGDYSDDHCYKVVYNGDLKRGSSYESVWVNFRRYREMTLVLDLIALFLPYDRLPKFV 287
 QY 296 KTELRLDVLTPDIYGVNNLNGYGT-----FSNIE--NYIRKRLFLDYLRHQFH-- 343
 Db 288 TQQLTREYTDALCTVPHPSFTSTWYNNMADPSFAIEAAVARNRHLDFLEQVITYSL 347
 QY 344 -TRQPGYGYGNDSEFNWVSGVYSTRPSISNDITTFPGNKSSEPVQMLFENGGEVYA 402
 Db 348 LSRMSNTQY---NMNMGGHKLERR-TIGCTLAIISQGSNTSINPV-TLPFTSDVYKT 401
 QY 403 VANNINLAVMSAYSGVTKVEFS-QYNDQDEASTQFYDSKRNVGAVSWDSIDOLPPEIT 461
 Db 402 ESLAGLNLFLTOPVNGVRVDFMFKVETPIASDNFYYPGAVIGIQGLDSSNELPEIT 461
 QY 462 DEPLEKGYSHQNLVVMCMFLMOGSRGTPVLVTHKSVDFPNMIDSKKITQPLVAVAKLO 521

DB 462 GQPNYESYHRLSHI--GLISASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLS 519

QY 522 SGASVYAGPRTGDDIICTENGSAATTYTPDVYSQKRYARIRHASTSQITFTLSLDG 581

DB 520 SGAAYVVRGPGFTGGDLIRNTGTGFDIRVYNINPFAQRYRIRASTDLDQFHTSING 579

QY 582 APNQAYVFDITKNGDLYTVNSFNLSAFSPPELSC--NNLOIGVYGLSAGKQVYIDKLE 639

DB 580 KAINQGNFSAIMNRGDELDTKTRTVGTTPPSFLDVOSTFTIGANNFSSGNEVYIDRIE 639

QY 640 FIPV 643

DB 640 FVPV 643

RESULT 14

C7AA_BACTU STANDARD; PRT; 1138 AA.

ID C7AA_BACTU

AC 003749;

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 30-MAY-2000 (Rel. 39, Last annotation update)

DE Pestigicidal crystal protein cry7Aa (insecticidal delta-endotoxin

DE CryII(a)) (crystalline entomocidal protoxin) (129 kDa crystal

DE protein).

GN CRY7AA OR CRYII(A) OR CRYIIIC.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI-TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RX Lambert B., Hofte H., Jansens K., Jansens S., Soetaert P., Peferoen M.,

RT "Novel Bacillus thuringiensis insecticidal crystal protein with a

RT silent activity against coleopterian larvae."

RL Appl. Environ. Microbiol. 58:2536-2542(1992).

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS

CC NATURAL FORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE

CC AFTER AN IN VITRO SOLUBILIZATION AND TRIPSIN ACTIVATION STEP.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF

CC THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-

CC TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@sib-sib.ch).

CC -----

CC EMBL: M64478; AAA2351.1; -

DR EMBL: A07236; CA00646.1; -

DR HSSP: P07130; IDIC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin.1.

DR Toxin: Sporulation.

SO SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1PAC CRC64;

Query Match 33.8%; Score 1152.5; DB 1; Length 1138;

Best Local Similarity 37.7%; Pred. NO. 4.9e-68;

Matches 255; Conservative 114; Mismatches 235; Indels 73; Gaps 19;

QY 1 MNPNRSEHDITKTENNEVPFNHQAETPNTLEADNKEFLMADNTAALUSS 60

DB 1 MNLNLMDYE-----DSNRLNLSNLTPTQKALSSIKMMNQDLSITERQPALSG 55

QY 61 TRKDVYQKISVVDLGVGCPFGALVSFTYTNLNTIWPSEDP--WKAEMEQLALMDQ 119

DB 56 NT--AINVYVSTGATLALGVGASFTTNFYLKTAGLMBENCKIMDEPMEVEALIDQ 113

QY 120 KIADYAKNKAALAELOGLONNVEDYVLSWSW---OKNPVSSRNPHSGRIEPLSQASH 176

DB 114 KIEEYRNKNAIEEDLDGSLADKYKALADNIGKDDDEALISVATERI-----IDSL 167

QY 177 FNSMPSFAISGEVLEFLTTTAAQANPHFLKDAQIYGEEMGEKEDIAPFYKQKLT 236

DB 168 FEFSMPSEFVGTGEYELPLTVYQAANLHALLRDSTLXGDKWGFQNNIENYNNQKRI 227

QY 237 OEYDHCYKMYVNGLDKIRGSSSEWVFNRRRMTLVLDLALFELYRLKPEVK 296

DB 228 SEYSDCHTKWNSGLSRNGSTYEQWIMYNNRRRMILMALDLAVFEPHDPRRYSMTS 287

QY 297 TELTRDVLDPF--YGVNMLRGYTFEFSNIEN-YIRKPHLPDYLRHIOPT-----RF 346

DB 288 TQLTREVTYDPLVSLISN--PDIGPESFQSMENYALFTPLVYLDLDELTYTKYAFSHEI 346

QY 347 QPGYTGNDSPNWSGNYSTRPSISNDIITSPEYKNSSEPVON--LEFNGEKYRARA 404

DB 347 QPDLF-----YMSAHKYSFKKSEQSN--LYTTGIYG-KTSGYISSGAVSFHNDIYRTLA 398

QY 405 NTLNLAWPSAVYSGVTKYEFQYNGQIDEASTQYDSCRNNGANVMSDIDLPETIDEP 464

DB 399 APSVAVVYPTQNYGVGEVGEYGVKGHVH RQDNKYD-----LYTSIDQLPPD--GEP 449

QY 465 LEKGYSHOLNVMCFIMOG---SRGTIPVLMTKHSVDFNMNIDSKITOLPLKAVKIQ 521

DB 450 IHEKTYHRLCHNATAFKSTPDYDNATIPFSMTIRHSAEYKRYRITPKITKIPAVKMKLD 509

QY 522 SGASVYAGPRTGDDIICTENGSAATTYTPDVYSQKRYARIRHASTSQITFTLSLDG 581

DB 510 DPSTVYKPGFTGGDLVGRSGTGYIGDIKATVNSLSQKYRVRATNV-----S 560

QY 582 APENQYDCK-----TINKGDTLTVNSFNLSAFSTPELSCNN--LQIGVYGL 627

DB 561 GOFNVTYINDKTLTQKFNVTYETTIGEGKDLVYGSFGYIEYSTTQFDPDEHKITLHSDL 620

QY 628 SAGDKVYIDKIEFIPVN 644

DB 621 SNNSFYVDISIEFIVD 637

RESULT 15

C9CA_BACTO STANDARD; PRT; 1157 AA.

ID C9CA_BACTO

AC 045733;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pestigicidal crystal protein cry9Ca (insecticidal delta-endotoxin

DE CryIXC(a)) (crystalline entomocidal protoxin) (130 kDa crystal

DE protein).

GN CRY9CA OR CRYIXC(A).

OS Bacillus thuringiensis (subsp. tolworthi).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI-TaxID=1442;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX STRAIN-BTS02618A;

RC MEDLINE-96141404; Pubmed-8572715;

RA Lambert B., Buysse L., Decock C., Jansens S., Plets C., Seey B.,

RA Seurlink J., Van Audenove K., Van Rie J., Van Vliet A., Peferoen M.,

RT "A Bacillus thuringiensis insecticidal crystal protein with a high

RT activity against members of the family Noctuidae."

RL Appl. Environ. Microbiol. 62:80-86(1996).

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD

CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,

CC PTELELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST

CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORKS. NO

CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO

CC BEETLE.

Search completed: January 10, 2003, 11:06:49
Job time : 16 secs

```
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: 237527; CAA85764.1; -
DR HSP: P07130; IDLC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin.1.
DR Toxin: Sporulation.
KM Toxin: Sporulation.
SO SEQUENCE 1157 AA; 129775 MW; C364391EF7FDEB8A CRC64;

Query Match 33.78; Score 1149; DB 1; Length 1157;
Best Local Similarity 37.58; Pred. No. 8.5e-68;
Matches 258; Conservative 126; Mismatches 230; Indels 74; Gaps 18;

Oy 1 MNPNNRSEHDTIKTTEENNEVPTNNOVPLAETPNPTLEDNLYKEFLRMFADNNTALD-- 58
Db 1 MNRKNOMEYELIDAPHCPCSDDDVRFPLASDPNALQNNKYKDYLOMTDEDYTDSTYNP 60
Oy 59 --SSTKDVIOKGISVVGDLGVGPEFGALVSFTNFINTIPSEDP--WKAFMEQVE 114
Db 61 SLISGSDAVQVATLVVGRITGALGVFSGQIYSFVOFLNTLMPVNDTAIMEAFMRQVE 120
Oy 115 ALMOQKLAADYAKKALAEGLQNNVDYSALSSMQKNPVSSRNPHSGRIRLEFSQAE 174
Db 121 ELVNOQITEFARNQALRLQGLGSENVYQSLQNLADNDNRN--LSVRAQFTALD 177
Oy 175 SHFNNSPSPFASISGEVLEFTTYAAQANTHLFLKDAQIYGEEMGEKEDIAEFYKRLK 234
Db 178 LDFVNAIFLPRVNGQVPLSYAQAANLHLLKLLKSLFGBOGFTQGEISTYIDROLE 237
Oy 235 LTOEYTDHCVKWYVGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLVYRLYPE 294
Db 238 LTAKYTYNCETWYNGLDRLRGTTESMLRYHQFRREMTLVLDVVALFPYDRLPYTG 297
Oy 295 VKTELTDVLDPIY-----GVNLRGCGT-----TFSNIEN-YIRKPHLFDYLARIQEHF 344
Db 298 SNPOLTREVTDPVFNPPANVGLCRWGNTPYNTFSELENAFIRPPLFLRLNLSLTISS 357
Oy 345 RFQPGYGNDSFNWYSGNVSTRPSIGSNDIITSPEYG-----NKSSEPVQNLFFN 395
Db 358 NRFP--VSSNPMQWMSGH--TLKRSYLANDSAVEDSGLTTRATINPGVDGTRIEST 413
Oy 396 GEKYRAVANTNLAVPSAVYSGTYKEF---SOYNDQIDEASTQYIDSKRNVGAVSWDS 452
Db 414 AVDFRSALI-----GIY-GVNRASFVPGCLFNCTSPANGCCHD-----LYDT 455
Oy 453 IDOLPP-ETTDEPLEKGYSHQNLVVMCFLMQ-----GSRGTIPVLTWTHKSYDFENMI 504
Db 456 NDELPPDESTGSS-----THRLSHVTFSPOTNAGSIANAGSVPIYVWTRDVLNNTI 510
Oy 505 DSKKITQLPLVKAYKLAGSASVAVGPRFTGDIIOCTENGSAATIVTTPVSYSOXYRAR 564
Db 511 TPNKITQLPLVKASAPVSGTTLKPGFTGGILRTTNGTFTGLRATVNSPLTQOYRLR 570
Oy 565 IHVASTQITFTLSLDGAPFNQYFEDKTINKGDTLYNSFNLSFST-----PFEISGN 618
Db 571 VRFASSTGNFSIRVLGCVSICGVALGSTMNGOELTFESEFTTREFFTTGGPNPFTTQA 630
Oy 619 N--LQIGVTGLSAGDKYIIDKIEFIYV 644
Db 631 QEILTVNAGVSTGGEYIIDRIETIYV 658
```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:03:39 ; Search time 38 seconds
(without alignment)
3491.956 Million cell updates/sec

Title: US-09-943-692-2
Perfect score: 3406
Sequence: 1 MNPNNRSEHDITKTENNEV.....TGLSGDKVYIDKIEFIVN 644

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP viirus:*
- 16: SP bacteriap:*
- 17: SP archaeap:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	652	2	Q9S6N9
2	1175	34.5	719	2	Q9F0P8
3	1155	33.9	719	2	Q93N75
4	1154	33.9	719	2	Q85796
5	1111	32.6	1228	2	Q93775
6	1108	32.5	1228	2	Q93N75
7	1088	31.9	645	2	Q9S603
8	1006.5	29.6	638	2	Q87654
9	988	29.0	1144	2	Q45745
10	980	28.8	1155	2	Q9F296
11	974.5	28.6	1118	2	Q9AM83
12	972	28.5	1155	2	Q93721
13	954.5	28.0	1180	2	Q9S5V8
14	944.5	27.7	1187	2	Q9L877
15	942.5	27.7	620	2	Q45720
16	942.5	27.7	1176	2	Q45736

17	935	27.5	1176	2	Q9RC30	Q9RC30 bacillus th
18	902	26.5	1118	2	Q9AM82	Q9AM82 bacillus th
19	891	26.2	1171	2	Q06894	Q06894 bacillus th
20	883.5	25.9	1176	2	Q9S514	Q9S514 bacillus th
21	882	25.9	1174	2	Q45749	Q45749 bacillus th
22	847	24.9	1177	2	Q45735	Q45735 bacillus th
23	842.5	24.7	1178	2	Q9R826	Q9R826 bacillus th
24	841	24.7	607	2	Q45721	Q45721 bacillus th
25	841	24.7	723	2	Q45737	Q45737 bacillus th
26	841	24.7	618	2	Q9S4B5	Q9S4B5 bacillus th
27	841	24.7	1177	2	Q03743	Q03743 bacillus th
28	839.5	24.6	618	2	Q03206	Q03206 bacillus th
29	839.5	24.6	1178	2	Q45768	Q45768 bacillus th
30	835.5	24.5	1160	2	Q937F9	Q937F9 bacillus th
31	826	24.3	1118	2	Q9AM81	Q9AM81 bacillus th
32	800	23.5	660	2	Q8R0V6	Q8R0V6 bacillus th
33	704	20.7	381	2	Q45740	Q45740 bacillus th
34	693.5	20.4	1280	2	Q8VUK9	Q8VUK9 bacillus th
35	684	20.1	1236	2	Q939Y3	Q939Y3 bacillus th
36	637	18.7	1128	2	Q9FDC0	Q9FDC0 bacillus th
37	613	18.0	1254	2	Q8VUL0	Q8VUL0 bacillus th
38	603	17.7	650	2	Q8VNX2	Q8VNX2 bacillus th
39	589.5	17.3	666	2	Q8VW62	Q8VW62 bacillus th
40	569.5	16.7	1155	2	Q9AM80	Q9AM80 bacillus th
41	526	15.4	688	2	Q8VNX1	Q8VNX1 bacillus th
42	504.5	14.8	1270	2	Q8VUL1	Q8VUL1 bacillus th
43	342.5	10.1	297	2	Q45789	Q45789 bacillus th
44	271	8.0	50	2	P81518	P81518 bacillus th
45	248.5	7.3	723	2	Q9EVR2	Q9EVR2 bacillus th

ALIGNMENTS

RESULT 1

Q9S6N9 PRELIMINARY: PRT: 652 AA.
ID Q9S6N9
AC Q9S6N9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Cry3Aa protein.
GN CRY3A.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
CC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BT22;
RA Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;
RT "A novel cry3Aa gene."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ237900; CAB41411.1; -.
DR HSSP: P07130; IDIC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 652 AA; 74035 MW; 544AE16E1DFF647 CRC64;

Query Match 100.0%; Score 3406; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.2e-220;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDITKTENNEVPTNHYQYPLAETPNPTLELDYKKEFLRTAANNTEALDSS 60
DB 9 MNPNNRSEHDITKTENNEVPTNHYQYPLAETPNPTLELDYKKEFLRTAANNTEALDSS 68
QY 61 TTKDVIQKISVVGDLGVGFPFGALVSFTYNFLNTIWPSEDPWKAFFMEQVEALNDOK 120
DB 69 TTKDVIQKISVVGDLGVGFPFGALVSFTYNFLNTIWPSEDPWKAFFMEQVEALNDOK 128
QY 121 TTDYAKNRALALQGLGNVEVYVSAISWQKNPVSSRNPSQGRIRLFSQAESHPFNS 180

Db 129 IADYAKNKAELQLOLONNVEDYVSSALSMQKNPVSSRNPHSGRIELESQAESHRRNS 188
 QY 181 MPFAISGEYELFTTYAOANTHLEFLKQOYIGEEMGYEKEDIAEFYKROLTOEYT 240
 Db 189 MPFAISGEYELFTTYAOANTHLEFLKQOYIGEEMGYEKEDIAEFYKROLTOEYT 248
 QY 241 DHCVKMYVNGDLKRGSSYESWVNFNRYRRMTLTVDLALFPLDYVRLYPRKEVKTETL 300
 Db 249 DHCVKMYVNGDLKRGSSYESWVNFNRYRRMTLTVDLALFPLDYVRLYPRKEVKTETL 308
 QY 301 RDVLDPYVGNLNGYTTSTNIENTIRKPHLEFDYLRHIOFHRPQGYGNDSEYVMS 360
 Db 309 RDVLDPYVGNLNGYTTSTNIENTIRKPHLEFDYLRHIOFHRPQGYGNDSEYVMS 368
 QY 361 GNYSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANTMLAVMPSAVYSGYT 420
 Db 369 GNYSTRPSIGSNDIITSPFYGNKSEPVONLEFNGEKYRAVANTMLAVMPSAVYSGYT 428
 QY 421 KVEFSQYNDQDEASTQTYDSKRNNGAVSWDSIDQLPEPTTDEPLEKGYSHQNLVYVNCFL 480
 Db 429 KVEFSQYNDQDEASTQTYDSKRNNGAVSWDSIDQLPEPTTDEPLEKGYSHQNLVYVNCFL 488
 QY 481 MGSRGITPVLWTNHSKVDFFNMDSKTIQPLVKAAYKQSGSVYAGPFTGGDIQC 540
 Db 489 MGSRGITPVLWTNHSKVDFFNMDSKTIQPLVKAAYKQSGSVYAGPFTGGDIQC 548
 QY 541 TENSSAATITVTPVYSOKYRAHIAVASTQITFTSLDGAPENOYFDTIKKGDITL 600
 Db 549 TENSSAATITVTPVYSOKYRAHIAVASTQITFTSLDGAPENOYFDTIKKGDITL 608
 QY 601 YNSFNLASFTSPFELSGNNLQIGVTLGASGDKYVYIDKIEFIPVN 644
 Db 609 YNSFNLASFTSPFELSGNNLQIGVTLGASGDKYVYIDKIEFIPVN 652

RESULT 2

Q9FOP8 PRELIMINARY; PRT; 719 AA.
 ID 09FOP8
 AC 09FOP8
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CRY1.
 GN CRY1.
 OS Bacillus thuringiensis.
 OG Plasmid pBTC19.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BTC007;
 RA Song F., Zhang J., Huang D., Li G.;
 RT "The cloning of a novel cryII gene from Bacillus thuringiensis
 strain..."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF211190; AAG43526.1; -
 DR HSSP: P02965; ICIT.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Plasmid.
 SQ SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match 34.5%; Score 1175; DB 2; Length 719;
 Best Local Similarity 39.0%; Pred. No. 1.7e-70;
 Matches 260; Conservative 126; Mismatches 234; Indels 46; Gaps 17;

QY 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPNPT---LEDLNYKEFLRMTADNNTA 56
 Db 1 MNLKPNPKHQSLSSNAKVDKATDSLK-----NETDIEKNNHEDFLRM---SEHS 50
 QY 57 LDSSTYDVIOKIGSVVGDLLGVGPPGALVSEYVNFNTIWP-SEDPKAFMEQVEA 115
 Db 1 MNLKNDKHKQSSNAKVDKISTDSLK-----NETDIEKNNHEDFLRM---SEHS 50

Db 51 IDPFVASTIQTIGIGIAGILGTLGVFPAGQIASLVSFTLIGELMPKGSQWEIFMEHVE 110
 QY 116 LMOCKIADYAKNKAELQLOLONNVEDYVSSALSMQKNPVSSRNPHSGRIELESQAES 175
 Db 111 LMOCKIADYAKNKAELQLOLONNVEDYVSSALSMQKNPVSSRNPHSGRIELESQAES 167
 QY 176 HFNNSMPFAISGEYELFTTYAOANTHLEFLKQOYIGEEMGYEKEDIAEFYKROL 235
 Db 168 LFOVKLPFAISGEYELFTTYAOANTHLEFLKQOYIGEEMGYEKEDIAEFYKROL 227
 QY 236 TQETTHCYKMYVNGDLKRGSSYESWVNFNRYRRMTLTVDLALFPLDYVRLYPRKEV 295
 Db 228 TQETTHCYKMYVNGDLKRGSSYESWVNFNRYRRMTLTVDLALFPLDYVRLYPRKEV 287
 QY 296 KTELTDVLTDPYVGNLNGYTTSTNIENTIRKPHLEFDYLRHIOFHRPQGYGNDSEYV 343
 Db 288 TQETTHCYKMYVNGDLKRGSSYESWVNFNRYRRMTLTVDLALFPLDYVRLYPRKEV 347
 QY 344 -TRFOPGYGNDSEYVNFNRYRRMTLTVDLALFPLDYVRLYPRKEV 400
 Db 348 LSRMSNTQY---MNMGGHRLER-TIGG--VLNSTGSGTNTSINPV-TLPFTSRDY 399
 QY 401 RAVANTMLAVMPSAVYSGYTKEFESQYNDQDEASTQTYD-SKRNNGAVSWDSIDQLPE 459
 Db 400 RAVANTMLAVMPSAVYSGYTKEFESQYNDQDEASTQTYD-SKRNNGAVSWDSIDQLPE 459
 QY 460 TTEPLEKGYSHQNLVYVNCFLMGSRGITPVLWTNHSKVDFFNMDSKTIQPLVKAAYK 519
 Db 460 TTEPLEKGYSHQNLVYVNCFLMGSRGITPVLWTNHSKVDFFNMDSKTIQPLVKAAYK 517
 QY 520 LOSGASVAGPFTGGDIQCENGSAAITVTPVYSOKYRAHIAVASTQITFTSLDGAPE 579
 Db 518 LOSGASVAGPFTGGDIQCENGSAAITVTPVYSOKYRAHIAVASTQITFTSLDGAPE 577
 QY 580 DGAPFNQYFDTIKKGDITLITNSFNLASFTSPFELSG--NNLQIGVTLGASGDKYV 637
 Db 578 NGKAINQGNFSATMNGEDLDYKTFRTVGFPTPFESFDVQSTFTIGAMFSSGNEVYIDR 637
 QY 638 IEFIPV 643
 Db 638 IEFIPV 643

RESULT 3

Q93NT5 PRELIMINARY; PRT; 719 AA.
 ID 093NT5
 AC 093NT5
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE CRY1A.
 GN CRY1A.
 OS Bacillus thuringiensis.
 OG Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song F., Zhang J., Gu A., Huang D., Li G.;
 RT "A novel CryIIA endotoxin..."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF373207; AAK66742.1; -
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SQ SEQUENCE 719 AA; 81225 MW; C629D72C44827241 CRC64;

Query Match 33.9%; Score 1155; DB 2; Length 719;
 Best Local Similarity 38.0%; Pred. No. 3.8e-69;
 Matches 252; Conservative 132; Mismatches 238; Indels 42; Gaps 15;

QY 1 MNPNNRSEHDITKTEN-NEVPTNHVOYPLAETPNPT---LEDLNYKEFLRMTADNNTA 56
 Db 1 MNLKNDKHKQSSNAKVDKISTDSLK-----NETDIEKNNHEDFLRM---SEHS 53

DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139621 MW; 3DA24ABF59C95C3 CRC64;

Query Match 32.6%; Score 1111; DB 2; Length 1228;
Best Local Similarity 38.2%; Pred. No. 7.7e-66;
Matches 255; Conservative 117; Mismatches 238; Indels 58; Gaps 21;

```

OY 1 MNPNNRSEHDTIKTTEENNEVPTNHVQYPLAETPNPTLEDNLYKEFLRMTADNTEALDSS 60
DB 1 MTSNRKNEENIINAVSHSQAQMD-----LLPDAIEDSLCIAEENNIIDPPVSA 48
OY 61 TTKDVIOGKISVVDLGVGPPGAGALVSFTYNTLNTWP--SEDPKAFMEQVEALMDQ 119
DB 49 ST---VQTGINAGRIIGLVGFAGQLASFSFLGELMPRGDQWEIIEHVEQLINQ 105
OY 120 KIADYAKKKAELAELOGLONNVEDYVSAIWSMOKNPVSSRNHSGRTRE--LFSC---AES 175
DB 106 QITENAKRTALARKLOGDSFRATQOQSLDLEWLEN--RDDARRSVLYTYQYIALEL 158
OY 177 FRNSMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGEXEKEDIAEFYKROLKLT 236
DB 160 FLNAMPLFAIRNOEVLPLMAYVQAANLHLRLDASLFGESEFLTSQELQRYRQYER 218
OY 237 QETDHCYKRYNNGDKLKGSSYESVWNRKRYREMTLYVLDIALFPLYDVRLYKEY 295
DB 220 RDSYSDCYEVNNTGLNSLRGTNAAVWRYNQFRDLTLGLVDLVALFPSYDRTYPIINT 278
OY 297 TELTRDVLTDPI--VGVN--NLRGYGT---TFSNIE--NYIRKPHLPDYLRHQFHRFQ 347
DB 280 AQLTRVYTDALGATGVNMAAMWYNNNAIPSAIEAARSPHLLDFLEQLTISA--S 337
OY 349 GYYGNDSEFNWGSNYSYSTRPSISNDITSPRYG--NKSEPVONLEFNGEKYRAVAN 405
DB 339 RSNSTRHMTYMGRTIOSRP--IGGG--LNTSTGATNTSINPV--TLRFASRDYRTESYA 393
OY 407 NLAVMPSAVY----SGVTKEFSQYNDQ--TDEAS---VQYDSKRKNVAVSMDSIDOL 456
DB 395 GVILM--GIYLEPIHGVPRVREFTNPONISDGTNYSQPYESP--GLOLKDSETEL 448
OY 458 PETTDEPLEKGYSHOLNYWCFMOSRGTIPLVLTWTHKSVFFNMIDSKRITQOLPLVK 516
DB 450 PETTERPNESYSHRLSHIGILQ--SRVNVPIYSMTHRSADRTWIGRNRTIQOLPMKA 506
OY 518 YLQSGASVYAGRFEGDIIQCTENGSAATYVTPDVYSOKYRARLHYASTSQITFT 576
DB 508 SELPGTGVYVRGPGFTGGIILRTNTGCGPIRVVNGPLTORVRIHGFYASTVDPDFV 566
OY 578 LSLDGAFFNQYFEDKTIKNGDITLYNSFNLASFSSTPELS--GNNIQIGVTGISADKYYI 634
DB 568 VSRGTTVNNFRRLKRTMNSGDELKYGNFVRAFTTTPFTTQIODIITRTISIGLSNGEYV 626
OY 636 IKIEIIPV 643
DB 628 IKIEIIPV 635

```

RESULT 6

O93NM5 PRELIMINARY; PRT; 1228 AA.
AC O93NM5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE CRI1BA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;

RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF368257; AA63251.1.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139666 MW; E86D9842341FB439 CRC64;

Query Match 32.5%; Score 1108; DB 2; Length 1228;
Best Local Similarity 38.3%; Pred. No. 1.2e-65;
Matches 256; Conservative 115; Mismatches 238; Indels 60; Gaps 22;

```

OY 1 MNPNNRSEHDTIKTTEENNEVPTNHVQYPLAETPNPTLEDNLYKEFLRMTADNTEALDSS 60
DB 1 MTSNRKNEENIINAVSHSQAQMD-----LLPDAIEDSLCIAEENNIIDPPVSA 48
OY 61 TTKDVIOGKISVVDLGVGPPGAGALVSFTYNTLNTWP--SEDPKAFMEQVEALMDQ 119
DB 49 ST---VQTGINAGRIIGLVGFAGQLASFSFLGELMPRGDQWEIIEHVEQLINQ 105
OY 120 KIADYAKKKAELAELOGLONNVEDYVSAIWSMOKNPVSSRNHSGRTRE--LFSC---AES 175
DB 106 QITENAKRTALARKLOGDSFRATQOQSLDLEWLEN--RDDARRSVLYTYQYIALEL 158
OY 176 FRNSMPSFAISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGEXEKEDIAEFYKROLKLT 235
DB 159 DELNAMPLFAIRNOEVLPLMAYVQAANLHLRLDASLFGESEFLTSQELQRYRQYER 218
OY 236 TOETDHCYKRYNNGDKLKGSSYESVWNRKRYREMTLYVLDIALFPLYDVRLYKEY 295
DB 219 TRDSYSDCYEVNNTGLNSLRGTNAAVWRYNQFRDLTLGLVDLVALFPSYDRTYPIINT 278
OY 296 KTELTRDVLTDPI--VGVN--NLRGYGT---TFSNIE--NYIRKPHLPDYLRHQFHRFQ 347
DB 279 SAQLTRVYTDALGATGVNMAAMWYNNNAIPSAIEAARSPHLLDFLEQLTISA--S 337
OY 348 PGYYGNDSEFNWGSNYSYSTRPSISNDITSPRYG--NKSEPVONLEFNGEKYRAVAN 405
DB 338 RSNSTRHMTYMGRTIOSRP--IGGG--LNTSTGATNTSINPV--TLRFASRDYRTESYA 393
OY 406 NLAVMPSAVY----SGVTKEFSQYNDQ--TDEAS---VQYDSKRKNVAVSMDSIDOL 456
DB 394 AGVILM--GIYLEPIHGVPRVREFTNPONISDGTNYSQPYESP--GLOLKDSETEL 448
OY 457 PETTDEPLEKGYSHOLNYWCFMOSRGTIPLVLTWTHKSVFFNMIDSKRITQOLPLVK 516
DB 449 PETTERPNESYSHRLSHIGILQ--SRVNVPIYSMTHRSADRTWIGRNRTIQOLPMKA 506
OY 517 AYKQSGASVYAGRFEGDIIQCTENGSAATYVTPDVYSOKYRARLHYASTSQITFT 576
DB 507 SELPGTGVYVRGPGFTGGIILRTNTGCGPIRVVNGPLTORVRIHGFYASTVDPDFV 566
OY 577 LSLDGAFFNQYFEDKTIKNGDITLYNSFNLASFSSTPELS--GNNIQIGVTGISADKYYI 634
DB 567 VSRGTTVNNFRRLKRTMNSGDELKYGNFVRAFTTTPFTTQIODIITRTISIGLSNGEYV 626
OY 635 IKIEIIPV 643
DB 627 IKIEIIPV 635

```

RESULT 7

O9S603 PRELIMINARY; PRT; 645 AA.
AC O9S603;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

[illegible]

Query Match	29.6%	Score 1006.5	DB 2	Length 638
Best Local Similarity	36.7%	Pred. No. 3e-59		
Matches 241	Conservative 110	Mismatches 227	Indels 79	Gaps 21
Query	25	VOYPLAEFNPTEEDNTYKEPLMTADNTEALD-----SSTKDYIQKISVYDGLGVY	80	
Db	16	VKPEITDDPNAGLONNNYKEVLTDTYDGTGSLNLSINTRDVLQGTGINVGRVLGL	75	
Query	81	GPEFGALVSEYTNFLNTWPSD--PMKAFMEVQVEMALDOKIADYAKKALAELOGLON	138	
Db	76	GVPEAGQLVTEYTFLLNQMLPTNNNAVMEAFMAQIBELIDRISQVNRNALDALTGIDH	135	
Query	139	NVEDYVALSSWOKNVSSRNPHSQIRIELFSQASHRNSPFAIS-GVE---VLPL	194	
Db	136	YNYEYLAALAEWLERNGARANLAFOR---FENLHQLEFVSQPSFGSGSERDAVALL	191	
Query	195	TTYQAANHLFLKPAQYIGEEGKEEDIAEFYRKQLKIQEYDHCKKVVNVGLDKL	254	
Db	192	TYVAQANLHLKLLKAEITYGARWGLNOGINLYFNAQDDRTQIYNNHCAYATNRGLENL	251	
Query	255	RGSSYESWVNFNRYRREMTLVLDLALPFLYDRLYKPEVTELRDVLTDPIYGVNVL	314	
Db	252	RGNTESWVNYHQFRREMTLAMDVALFPYVNLQVPGNANPOLREIYTTDVPV--FNPP	310	
Query	315	RGYG-----TFPSNLEN-YIKKPHLFDLHRQFHTRPQPGYGGDSFNYSNGY	363	
Db	311	ANGGLCRMNWNNPYMFESELENTEFIRPHLEDRLNLSLTINSHRP--ISSFNMDYAGH-	367	
Query	364	VSNRPISGSDILITSPYKSSPEVQ-NLEFNGEKYRAVA-----NTNLAVV-----	411	
Db	368	TLRRSTMNNSAAVOEDSYGATTSTRTYTINGVGNTRINESTAVDFRGLLGIVGVNHSF	426	
Query	412	-PSAVSGLVKVFEQYNDQTDASTQTYDSKRVGAVS-WDSIDLPL-BETJDEPLEKG	468	
Db	427	VPGLGLFGCTL-----SPANAGCRNLHDPDEPLBENNNSP-----	462	
Query	469	YSHQNLV--MCL--MGS---RGITPVLTWTHKSVDFENMIDSKITQLPYLKAKLQ	521	
Db	463	-SHLSHTPLSELTLDQAGSIRNSGAVPLVYMARQDIDLNTTANNTIQLPLVKASEA	521	
Query	522	SGASVAVGPRGTGDIIDTCENGSAATLYTVPDVYSOKYRARIHVASTQIYPTTSLDG	581	
Db	522	AGITVAVGPGGTGDIILRRISAGLGIIRVAVNSPLQRYRVRRYASTJDFNFYVIRGG	581	
Query	582	APFNQYFDTKINKGDLITYNSFNLSASFPEEL--SGNNLQIGVTLGSLAGDKYID	636	
Db	582	TYVNNFTFPRTMNGQESRSESYVTREFSNFSFNLOJDTLRLTVQSFSSGQGVYVD	638	

DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 GN CRYX GENE.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94085596; PubMed=8262221;
 RA Shevelev A.B., Svaritsky M.A., Karasin A.I., Kogan Y.N.,
 RT "Primary structure of the cryX**--the novel Delta-endotoxin-related
 RT gene from Bacillus thuringiensis ssp. galleriae."
 RL FEBS Lett. 336:79-82(1993).
 DR EMBL: X75019; CAA52927.1;
 DR HSSP: P07130; IDC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 FT NON_TER
 SQ SEQUENCE 1144 AA; 12939 MW; 7D28594A19C4B05 CRC64;

Query Match 29.0%; Score 988; DB 2; Length 1144;
 Best Local Similarity 35.4%; Pred. No. 1.3e-57;
 Matches 229; Conservative 117; Mismatches 237; Indels 64; Gaps 17;

41 NYKFLMTADNNTA-LDSSTKDYIOGIVGDLGVGFPFGALVSFTYNTLMTI 99
 19 SYKDYLMKSGDYIDYINPGVNRGLQIDIVAVVAGLGPVGILTFELSGEL 78
 100 WPEDEP--WKAREVQYALMDKDIADYAKKLAELQGLQNNVEDYVSALSSWQNPVSS 157
 79 WPSNDAAVWEALFEQMEELIEQRIISDQVVRALDGLTQIYVYQYQILALEKMEERP--- 135
 158 RNHSQGRRELFSQASHFRNSMPSFAISG-----YEVLETTYQAQANHLTLDAQ 212
 136 -NGVRANLVLQRFELHAFVSSMPSFG-SGSGSGRFAQOLVYVQAANHLTLDAE 193
 213 IYGEKGYKEDIABEYKQKL-TOEYTDHCWKVYVNGDLKSGSYESVWVFNRARE 271
 194 KTGARWGLESQIGNLYFNELOTRTDYTNHCYNVANGLAGLGTSAESLKHQRR 253
 272 MFLTVLDLALPLVDVRLYKPEVKTLELDYLDPIYVANN-----LRGYGT- 319
 254 ATLAMDIALPLPYNTRRYPLAAMPOLTRREYTDPL-GVPSSESSLPELRLCRLMOETS 312
 320 --TFSTNEN-YLRPHLEDYLHRIQFHTRFQGYGNDSEFYMGSNVYSPRPSIGSNDII 376
 313 AMFNSLLEWALISPHLDITNNLITGYFSVHLTNQLEGMWIGHVTSLSLASCFTTV 372
 377 TSPFGKNSSEPVQMLENGEKYRAVANMLAY-WPSAVYSGVYKVEF-----SOY 427
 373 LRRNKGSTTS-IVNYFSENDRDVYOINTRSHTGFGFQNAFLFGITRAQFPGGTYSVOR 421
 428 NDQTEASTQYVDSKRNKGAWSMDSIDQLPETTDEPLEGYSQQLVYVWCFL-----MQ 462
 432 NALTCEQ-----NYSIDELPSLDNEPLSKYSYRSHITSYHRLVLTID 477
 483 GSR---GTIPVLTWTHKSVDFNNIDSKKITQLPLVAKYKLSGASVAVAPRFTGGDIQ 539
 478 GINISGMLPTVYVWTHRDVLTNTTADRTQLPLVKSFEIPAGTIVVRPGCTGGDIAR 537
 540 CTENGSAATIVTPDVASOKYRARIHASTSQTFTLSLDGAPNOYVYDKTINKGDL 559
 538 RTGVTGFTINRTTAPLQRYRIRFRFASNTNLFIGIRGDRQVNVFDFGRTMNGDEL 597
 600 TYNSENLASFSTPELSENNLQIGV--TGLSAGKVIYIDIEFIPV 644
 598 RYSPATREFPTTDFNQPOELLISVFANNAASAGEVYFDEITIPV 644

RESULT 10
 ID 09F296 PRELIMINARY; PRT; 1155 AA.
 AC 09F296;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Meza-Basso L.A., Theodoruz C.,
 RT "Cloning and expression of a delta endotoxin gene from a Chilean
 RT native Bacillus thuringiensis strain."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U94191; AAG16877.1;
 DR HSSP: P02965; ICY.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SQ SEQUENCE 1155 AA; 130557 MW; 5D69E3E2F527749D CRC64;

Query Match 28.8%; Score 980; DB 2; Length 1155;
 Best Local Similarity 33.9%; Pred. No. 4.4e-57;
 Matches 225; Conservative 124; Mismatches 231; Indels 84; Gaps 19;

2 NPNNSEHDTITTEENEVYTNHVQYPLAETPNPLTDLNKEFLMTADNNTALDST 61
 4 NPN-----INECIPYNCLIS-----NPEVEVLGE---RIETGYTPIDISLSL 42
 62 TKVDYIOGIVGDLGVGFPFGALVSFTYNTLMTI-----PSEDPKAFMQLV 117
 43 TOPLSEVPAGVGLV-----DITLFGFSQ--WAFVQIQIL 84
 118 DQIADYAKKLAELQGLQNNVEDYVSALSSWQNPVSSNPSQGRIRLEFSQASHF 177
 85 NORIEEFARNAQMSRLQESNLYQYASPREWEADPT--NPALREEMRIQFDMNSAL 141
 178 RNMSPEFASGVEVLETTYQAQANHLFLKDAQIYGEKGYKEDIABEYKQKLQ 237
 142 TTAIFLEAQNQVPLLSVYQVQANHLSTVLDVSVFGQRFMAAINSRYNDTLRLIG 201
 238 EYTDHCWKVYVNGDLKSGSYESVWVFNRAREMTLTVLDLALPLVYVRLPKVK 297
 202 NTDHAYNRVNTGLERWVGPDSDRMIRYNQPRRELITLVLDIVSLFPNYDSKRTPIRTVS 261
 298 ELTRVLDPIYGVNNLKG-YGTFFSNIENTYIRKPHLEDYLHRIQFHTRFQGYGNDSE 356
 262 QLTREIYTNPV--LENFSGSFRSGAQIEGSIIRSPHMDLINSITITYTDAHREY----- 314
 357 NWSGNYVSTPRSGSNDIITSPFYGNK--SEEPQNLNLFN-GEVYRAVANMLAWPSSA 414
 315 -YWSHQIMASPVGSGEETFPPLGTWGNAPQORIVAOIGGVYKRTLSST---LYRRP 370
 415 YVSQYKVEFQYNDQTEASTQYVDSKRNKGAWSM-----DSIOLPETTDEPLEG 468
 371 FNIGINMOQLSVL-DGTFEA---YGTSSNLPSAVYKKSQTVSDLEIPQNNNVPRQG 425
 469 YSHQNTYACLQMGSKRTI-----PVLVLTWTHKSVDFNNIDSKKITQLPLVAKYKLSG 523
 426 FSHRLSHVSMRSGFSMSVSIIRAPMFSWTHRSAEFNNTIIPSSQITQPLFKSTNLGSG 485
 524 ASVAPRFTGGDICTENGSAATIVTPDVASOKYRARIHASTSQTFTLSLDGAP 583
 486 TSVKGRFTGGDLIRKTSQQLSTLVNVTAPLSQRYRIRYASTTMDQFTSIDGR 545
 584 FNQYFDTINKGDTLTVNSENFLASFSTPELSENNLQIGVGLSA-----GDKYIDKI 638
 546 INQGNFATMSSGSLGSGSFRVYVGTTPPNFNGS---SVFLSAHAYVNSGNEVYIDKI 602
 639 EFIP 642

Db 603 EFVP 606

RESULT 11

09AM83 PRELIMINARY; PRT: 1118 AA.

AC 09AM83: 01-JUN-2001 (TREMREL. 17, Last sequence update)
 DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE Insecticidal crystal protein BPRX24.
 OS Bacillus thuringiensis serovar kunthlarx24.
 OC Bacteria: Firmicutes: Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 NCBI_TaxID=147284;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Nagarathnam P., Xavier R., Jayaraman K., Murugan V.;
 RT Characterization and full-length sequencing of insecticidal crystal
 RT protein (cryI) of novel Bacillus thuringiensis subsp. kunthlarx24 and
 RT its specific toxicity towards three economically important pests;
 RT Spodoptera litura, Helicoverpa armigera and Plutella xylostella.";
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF327924; AAK14336.1; -
 DR HSSP: P02965; 1C1Y.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 SO SEQUENCE 1118 AA; 12681 MW; 33DA5B8C2CDF059D CRC64;

Query Match 28.6%; Score 974.5; DB 2; Length 1118;
 Best Local Similarity 34.1%; Pred. No. 9.8e-57;
 Matches 221; Conservative 125; Mismatches 230; Indels 73; Gaps 18;

QY 17 NNEPTNHNQVPLAETPNPLEDLNTYKEFLMRTADNTEALDSTTKDYOKGISVYGD 76
 DB 8 NECIPTNCL-----NPEYVLGE-----RIETGYPIIDISLVLQPLSEVPAGGFV 57
 QY 77 LGVVFPGGALVSYTNFTNTIW-----PSEDPKAMEQVEALMDOKIADYAKKALAE 132
 DB 58 LGLV-----DIINGIFGPGSQ--WDAPLVQIEQLINQRIEFANQAIISR 99
 QY 133 LOGLONNVEDYVSLSSWQKPNVSSRNPHSOGRIELFSAQESHFRNSMPSAISGEVL 192
 DB 100 LEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNMNSALTYAIPLEFAVQNOVP 156
 QY 193 FLTYYAQAANTHFLKDAQIYGEEMGYEKEDIAEFYKROLKQETDHCVKRYNGLD 252
 DB 157 LLSYVQANLHLVLYNDVYFGQRKGFDAATINSRINDLRLIGNTTDAHVRNTGLE 216
 QY 253 KLRGSYSESVNFRNRRKMTLVLDIALFPLVDRLYPEKRETELTDVLDPIVGN 312
 DB 217 RVMPDSDHMYRIYNOFRRELTLYLDIVSLPNDSTRYPPIRTYSQTLREIYTPV--LE 274
 QY 313 NLRG-YGTFENINENYIRKPHLFYLRHQFTRFOGYNDSPFNWMSGVYSTRSIG 371
 DB 275 NFDGSFRGSAAGIGSISRPILMDILNSTIYTAHREY-----YWSGHQIMASPVGE 328
 QY 372 SNDITTSFPGYGNK--SEPVQMLEFN--GEKYRAVANTMLAVPASYGVYKVFESYOND 429
 DB 329 SCPEPTPLVYGTMGNAQORIVAOLOGGYRTLSST--LYRRPFGINQNOQLSVL-D 384
 QY 430 QTEASTQYDSKRVAVSW-----DSIDQLPETTDEPLEGYSHQLTNYMCFLMOG 483
 DB 385 GTEFA---YGTSSMLPAAVYRKSGTVDLDEIPONNNVPPRGFSHRLSHVSMFRSGE 440
 QY 484 SSGT-----PVLWTHSVDFPNMIDSKKITOLPLVYKAYLOGSGASVAVAPRFGGII 538
 DB 441 SNSSVITIRAPFWSIHSAEENITPSSQITQIPLTSTNLGSGTSYVKKPGTGGDIL 500
 QY 539 QCTENGSAATVYTPDVYSQKYRARIHASTQITFTSLDGAFFNOYEDKTIKNGDT 598
 DB 501 RRTSGOISTLRVNTATLALSGQRVIRKASTTNTQFHTSIDGRINQNGNSATWSSGN 560

QY 599 LTYNSFNLASFTPELNGNNLQIGVTGLSA-----GDKVYIDKIEFIP 642
 DB 561 LQSGAFMTVGTFTTFPNFSNGS---SVFTLSAHVFNSGNEVYIDRIEFVP 606

RESULT 12

093721 PRELIMINARY; PRT: 1155 AA.

AC 093721: 01-DEC-2001 (TREMREL. 19, Created)
 DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
 DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
 DE Crystal protein CryIAb16.
 GN CRYIAB16.
 OS Bacillus thuringiensis (subsp. israelensis).
 OC Bacteria: Firmicutes: Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 NCBI_TaxID=1430;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Yu J., Tan L., Wu D., Pang Y.;
 RT "Molecular characterization of a silent gene encoding a 130-kilodalton
 RT crystal protein from Bacillus thuringiensis subsp. israelensis.";
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF375608; AAK55546.1; -
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 SO SEQUENCE 1155 AA; 130747 MW; 7F0C98BE0100C7698 CRC64;

Query Match 28.5%; Score 972; DB 2; Length 1155;
 Best Local Similarity 33.7%; Pred. No. 1.5e-56;
 Matches 224; Conservative 123; Mismatches 233; Indels 84; Gaps 19;

QY 2 NPNRBEHDTIKTENNENPTNHNQVPLAETPNPLEDLNTYKEFLMRTADNTEALDST 61
 DB 4 NPN-----INECIPTNCL-----NPEYVLGE-----RIETGYPIIDISLVL 42
 QY 62 TKDVIQGISVVDLGVYFPGGALVSYTNFTNTIW-----PSEDPKAMEQVEALM 117
 DB 43 TQFLSEPVPGAGFVGLV-----DIINGIFGPGSQ--WDAPLVQIEQLI 84
 QY 118 DQIADYAKKALAELOGLONNVEDYVSLSSWQKPNVSSRNPHSOGRIELFSAQESHF 177
 DB 85 NORIEEFARQAIISRLGSLNYQIYAESFREWEADPT--NPALREEMRIQFNMNSAL 141
 QY 178 RNMPSPAISGEVPLFTYYAQAANTHFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQ 237
 DB 142 TTAIPLEFAVQNTAVPPLLSYVQAVNHLVLYFGQRKGFDAATINSRINDLRLIG 201
 QY 238 EYTDHCVKMYNGLDKLRGSYSESVNFRNRRKMTLVLDIALFPLVDRLYPEKRE 297
 DB 202 NYTDHAVRWYNTGLERWGPDSRDWIRYNOFRRELTLYLDIVSLPNDSTRYPPIRTVS 261
 QY 298 ELTRDVLDPDIVGNVNLRG-YGTFENINENYIRKPHLFYLRHQFTRFOGYNDSPFN 356
 DB 262 QLTREIYTPV--LENFDGSFRGSAAGIGSISRPILMDILNSTIYTAHREY----- 314
 QY 357 NYMSGNVSTRPSIGSNDITTSFPGYGNK--SEPVQMLEFN--GEKYRAVANTMLAVP 414
 DB 315 -YWSGHQIMASPVGEFSTPEPTPLVYGTMGNAQORIVAOLOGGYRTLSST--LYRRP 370
 QY 415 VYSGVTKEVESQINDQTEASTQYDSKRVAVSW-----DSIDQLPETTDEPLENG 468
 DB 371 FNIGINNQQLSVL-DGTEFA---YGTSSMLPAAVYRKSGTVDLDEIPONNNVPPRG 425
 QY 469 YSHQNTVMCFLMOGSGRGT-----PVLWTHSVDFPNMIDSKKITOLPLVYKAYLO 523
 DB 426 FSHRLSHVSMFRSGFSNVSITIRAPFWSIHSAEENITPSSQITQIPLTSTNLGSG 485
 QY 524 ASVAGPRFTGGDITQCTENGSAATVYTPDVYSQKYRARIHASTQITFTSLDGAFFNO 583

Db 486 TSVVKGCFGTGDLRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGR 545
 QY 584 ENQYEDKTKNGDITLYNSFNLSSTPELSENNLQIGVTGLSA-----GDKYIDKI 638
 Db 546 INQNFSAITWSSGSLQSGSFRTVGTTPNFNSNGS---SVFTLSAHVNSGNEYIIDI 602
 QY 639 EFIP 642
 Db 603 EFVP 606

RESULT 13

Q95SV8 PRELIMINARY; PRT; 1180 AA.

AC Q95SV8; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE BT84A1 crystal protein.
 GN BT84A1.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T84A1;
 RA Nagamatsu Y.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T84A1;
 RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
 RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus
 thuringiensis subsp. dendrolimus T84A1.";
 RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T84A1;
 RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
 RT "A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
 thuringiensis.";
 RL Agric. Biol. Chem. 48:611-619(1984).
 DR EMBL; AB026261; BAA77213.1; -
 DR HSSP; P02965; ICIV.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SO SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DCE62D CRC64;

Query Match 28.0%; Score 954.5; DB 2; Length 1180;
 Best Local Similarity 33.7%; Pred. No. 2.4e-55;
 Matches 227; Conservative 118; Mismatches 224; Indels 105; Gaps 20;

QY 2 NPNRSEHDTITENNEVPYTHVOYPLAETPNPTLEDLNTKEFLRTADNNTALDST 61
 Db 4 NPN-----INCEIPYKCLN-----NPEVEVLGCE---RIETGTPIDISL 42
 QY 62 TKDVTKGIVSGDILGYVGFPGALVSTNPNNTIW-----PSEDPKAFMEQVEALM 117
 Db 43 TQFLSEVPQAGFVLGLV-----DIITGJFGPSQ--WDAFLVQIOL 84
 QY 118 DOKIADYKNAALALQGLQNNVEDYVALSSMOKNPVSSRNPHSOGRIELFSQAESHF 177
 Db 85 NORIEEFARNAISRLBELSLMLYOYIAESFREWEDP---NPLAREMRIOFDMNSAL 141
 QY 178 RNSMPSFISGTEVLELTYYAQAANTHLFLKDAOIYGEEMGVEKEDIAEFYKRLQTLQ 237
 Db 142 TTAIPLFAVQVQYVPLSLVYQAAHLHSLYRDVSVGQRMGFPAATINSRYNDLTLIG 201
 QY 238 EYTDICVQWYVGLDKLGGSSYSESVNRRRREMTLYVDLLFLPYLYRKYREKYKT 297
 Db 202 NYTDAVAMVMTGLERWGPDSRDMVRYNQPRRLTLVLIDIVALFSNYSRRYPIRTVS 261

QY 298 ELTRDVLDPPIVGVNNGYGTFT-----SNLENYIRKPHLFDYLHRIQFHTRFQPGYCN 353
 Db 262 QLTREIYNPV-----LENFDSFRGAORIEQNRQHLNRIITYDVHNG----- 312
 QY 354 DSEFNWAGNYSTRPSISNDITTSPEYGNK--SEPPVONLEFNEKEKYRAVANTLAWVP 412
 Db 313 --FNWSGHQTASPVGSGPEFAFLPGNAGNAPVYLVLTGIGIFRTLS----- 362
 QY 413 SAVY-----SG-----YKVEFSQYNDOTDEASTQYTDKSRNNGAVSWSDIDLP 458
 Db 363 SPLRYRIILGSGPNNOELFVLDGTEEFSPASLTINLPST---IYRQRTV--DGLDVIYP 416
 QY 459 ETTDEPLEKGYSHOLNYMCFMCGSRGTI-----PYLTWTKRGVDFPNMDSKRIQLP 513
 Db 417 QDNVPPRAGFSHRLSHT--MLSGAGAVYTLAFTPSWQHRSAERNNIIPSSQITQIP 474
 QY 514 LVKATKLOSAGSVAGPFTGGDIIIOCTENGSAATYVDPVYSQRYRARIHYASTSQI 573
 Db 475 LTKSTNLGSGTSVWGPFGTGDILRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNL 534
 QY 574 TETLSLDGAPNQQYFEDKTKNGDITLYNSFNLSSTPELSENNLQIGVTGLSA----- 629
 Db 535 QFHTSIDGRPNQNFSAITWSSGSLQSGSFRTVGTTPNFNSNGS---SVFTLSAHVN 591
 QY 630 -GDKYIDKIEFIP 642
 Db 592 SGNEYIDRIEFVP 605

RESULT 14

Q9L877 PRELIMINARY; PRT; 1189 AA.

AC Q9L877; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Toxin Cry1Ca6.
 GN CRY1Ca6.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_Taxid=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A2-F;
 RA Yu J., Pang Y., Li J.;
 RT "Cloning and sequence analysis of the cry1Ca6 gene from Bacillus
 thuringiensis, strain A2-F.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF215647; AAF37224.1; -
 DR HSSP; P02965; ICIV.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 SO SEQUENCE 1189 AA; 134685 MW; 98F8C1D978DF9451 CRC64;

Query Match 27.7%; Score 944.5; DB 2; Length 1189;
 Best Local Similarity 35.2%; Pred. No. 1.1e-54;
 Matches 234; Conservative 113; Mismatches 226; Indels 91; Gaps 24;

QY 16 ENNEVPYTHVOYPLAETPNPTLEDLNTKEFLRTADNNTALDSTTKVYOKGISVGD 75
 Db 3 ENNO--NOCIPYKCLNPEEVLIDG-----RISTNSSIDISLTVQPLVSNFVGGF 55
 QY 76 LLGVGFPGFGLAVSYTNELNTIMPSEDPKAFMEQVEALDQKADYAKKALAELOG 135
 Db 56 LVGLIDPVMG-----IVGPSQ--WDAFLVQIOLINERIAERARNAALANLGC 101
 QY 136 LQNNVEDYVALSSMOKNPVSSRNPHSOGRIELFSQAESHFRNSPSPASIGYEVLELT 195
 Db 102 LGNNFNVIYEAFAWEDEDP---NNPATRTYRIDRFRILDLGLERDIPSRISGFEVPLLS 158
 QY 196 TYQAAANTHLFLKDAOIYGEEMGVEKEDIAEFYKRLQTLQDEYIDHCKWYNVGLDKIR 255

Db 159 VVAQANLHLAILRDSVIFGERMGVTTINVENYNNLRIRHIDEYADHCANTYNGLINLP 218
 QY 256 GSSYESVAVNNRKRREKTLTVLDLALFELYDRLYPKEVKTLDVLTDPVGVN-NL 314
 Db 219 KSTYQDMITTYNNRLRLDLTVLDIAAFPNYDNRKRPDIQVGLTREVYDPLINPOL 278
 QY 315 RGYG--TTFENIE-NYIRKPHLEDYLRHQFHTRFQPGYGNDSFN-----YSSGNYVS 366
 Db 279 QSAQALPTEFVWESSALRNPHLDLNNLTFT-----DPSVGRNFYWGHRVTS 329
 QY 367 RPSIGNDITSPFYGNKSS-EFVQNLNENGKRYAVANTNLAV-----WPSAVYS--GV 419
 Db 330 SLIGGGN--ITSPYIGLEANQEPSPSTENG-PVFRILSPILRLAQGPAPAPFNLRCY 386
 QY 420 TKVEFSQYNDQTEASTQYIDSKRNAGVSWDSIDLPETTPDEPLEKGYSHQNTVCF 479
 Db 387 EGVEFS-----TPNSFTY--RGRQTV--DSELTPEPDNSVPPREGYSHRL---CH 431
 QY 480 LMGSGRTIPVL-----THKSVDFENMIDSKKITOLPLVKAYLQSGASVYAGPRT 533
 Db 432 ATYQASGRTIPVLTVTVFSTHRSATLNTIDERINQPLVGFVWGTSTVTPGFT 491
 QY 534 GGDICTENGSAATYVTPDVYSQKRYARIHASTQITFTLSLDCAPN-----585
 Db 492 GGDILRNRTGDPVSLQVNNINSPITQYRLRFYAS-SRDARYIVLGAATGCVGVY 550
 QY 586 QYFDKTKNGDLYTNSFNLASFSPPFELSGNNLQIGVT-----GISACKVYIDK 637
 Db 551 NMDLQTMGEINLMTSTFRYTDPSNPFSEFRANDILGISERPLFGAGISSGE-LYIDK 609
 QY 638 IEFI 641
 Db 610 IEIT 613
 RESULT 15
 045720 PRELIMINARY; PRT: 620 AA.
 AC 045720;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE CRYIA(a) (Fragment).
 GN CRYIA(a).
 OS Bacillus thuringiensis.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RP [1]
 RC STRAIN-NRD-12;
 RA MEDLINE-95386467; Pubmed-7657602;
 RA Masson L., Lu Y.J., Mazza A., Brousseau R., Adam M.J.;
 RT "The CRYIA(C) receptor purified from Manduca sexta displays multiple
 RT specificities";
 RL J. Biol. Chem. 270:20309-20315(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRD-12;
 RA MEDLINE-95231292; Pubmed-7715447;
 RA Masson L., Mazza A., Gringorten L., Baines D., Anellunas V.,
 RT "Specificity domain localization of Bacillus thuringiensis
 RT insecticidal toxins is highly dependent on the bioassay system";
 RL Mol. Microbiol. 14:851-860(1994).
 DR EMBL: U43605; AAA86265.1; -;
 DR HSSP: P02965; ICIX.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 FT NON_TER 1
 SQ SEQUENCE 620 AA; 69428 MW; 4571A095E565EDE CRC64;

Query Match 27.7%; Score 942.5; DB 2; Length 620;
 Best Local Similarity 33.4%; Pred. No. 5.7e-55;
 Matches 225; Conservative 118; Mismatches 226; Indels 105; Gaps 20;
 QY 2 NNNNREHDTITTTENNENPTNHQVPLAEFNPFLDELNAYKEFLRMADNTEALDSSST 61
 Db 4 NFN-----INCEIPNCLN-----NPEVEVLGE--RIETGTPIDISL 42
 QY 62 TRDVIOKGISVVDLIGVGFPPGALVSFYTNFNTMT-----PSEDWKAEMEVEALM 117
 Db 43 TQFLISEFPGAGFVLGLV-----DIIMGIFGPGQ--WDNFVQIDBLI 84
 QY 118 DOKIADYANKKLAELQIGNNVEDYVSAIISWQKNPVSSRNPHSGNIRELFSQAESHF 177
 Db 85 NORIEEFARNQAIISRLGSLNLYQIYAESFREMADEPT--NPALREMRQIFNDMSAL 141
 QY 178 RSMSPFASGEVFLFTYQAANTHLFLKDAQIYEBEGYKEDAEFYKRLKLTQ 237
 Db 142 TTAIFLLAVQNTQVPLSTYVOANLHLSLVLDVSVFGQRMGFDAATINSRYNDLTRLIG 201
 QY 238 EYTDHCQKKNYNGDLKRLNGSSYESVWNNRYRRENTLVLDLALFELYDRLYPKEVKT 297
 Db 202 NYTDVAVRMYNTGLBRWMPQSDRWVRVYNGFRELTLVLDLVALFSNYDSRRYPIRTVS 261
 QY 298 ELTRDVLDPYGVNNLKCYGTF-----SNIEYTRKPHLEDYLRHQFHTRFQPGYGN 353
 Db 262 QLTRELITMPV-----LEFDFSGFRMAQRIEQNRPHLMDILNSITITVDVHRC--- 312
 QY 354 DSEFNWGSQYVSTRPSIGNDITSPFYGNK--SSEPVQNLNENGKRYAVANTNLAVWP 412
 Db 313 --FNWSGHQITASPVGFGPEFAFPFLFGNAGNAPVVLVSITGLGIRTLN----- 362
 QY 413 SAVY-----SG-----VTKVEFSQYNDQTEASTQYIDSKRNAGVSWDSIDOLP 458
 Db 363 SPLYRRIILGSGPNNQELFVLDCTEFSPASLTNLPST-----IYRQRTV--DSLIDVLP 416
 QY 459 ETTDEPLEKGYSHQNTVYVCMFLMGSSRGTT-----PVLWTNHSVDFFNMIDSKKITOLP 513
 Db 417 QDNSVPPRAGFESHRLSHVT--MLSOAGAVVYLTRAPTFSMQHRSAFNNIIPSSQITQIP 474
 QY 514 LVKAYKLGASGVAVGPRPTGDIQCTENGSAATYVTPDVYSQKRYARIHASTSQI 573
 Db 475 LKSTNLSGSGISVKGPGFTGDIKRTSPGQISTLRNITAPLSQRYRIRIRYASTNL 534
 QY 574 TPTLSLDGAPFNQYFDKTKNGDLYTNSFNLASFSPPFELSGNNLQIGVTGLSA----- 629
 Db 535 QFHTSIDGRPIQGNFASMTSGSNLQSGSFRTVGFTTTPNFSNGS---SVFTLSAHYFN 591
 QY 630 -GDXYIDKIEFIP 642
 Db 592 SCNEVYIDRIEIEVP 605

Search completed: January 10, 2003, 11:07:35
 Job time : 42 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 14:27:10 : Search time 40 Seconds
(without alignments)
2145.335 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644

Sequence: 1 MNPNNRSEHHTITTEENEV.....TGLSADKVIYIDKIEFIPVN 644

Scoring table:

Gapop 60.0 , capext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_101002:*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	644	9 AAP70085	Sequence of toxin
2	644	100.0	644	9 AAP82487	Delta endotoxin en
3	644	100.0	644	10 AAP94679	Amino acid sequenc
4	644	100.0	644	10 AAP95585	M-7 crystal toxin.
5	644	100.0	644	14 AAP39751	Delta endotoxin.
6	644	100.0	644	15 AAR56697	CYIIB insecticida
7	644	100.0	644	15 AAR56698	CYIIB insecticida
8	644	100.0	652	20 AAY23214	Amino acid sequenc
9	597	92.7	597	17 AAW00334	Bacillus thuringie
10	597	92.7	597	21 AAY69666	Wild-type Bacillus

11	595	92.4	610	11 AAR05537	Synthetic Bacillus
12	595	92.4	610	17 AAW00333	Bacillus thuringie
13	595	92.4	610	21 AAY69667	Bacillus thuringie
14	590	91.6	956	12 AAR15784	B. thuringiensis to
15	590	91.6	1100	17 AAR15783	B. thuringiensis to
16	543	84.3	644	17 AAR99960	B. t. coleopteran
17	543	84.3	644	18 AAW34811	Novel CryIIIA muta
18	543	84.3	644	18 AAW34812	Novel CryIIIA muta
19	543	84.3	644	18 AAW34813	Novel CryIIIA muta
20	543	84.3	644	18 AAW34814	Novel CryIIIA muta
21	543	84.3	644	18 AAW34815	Novel CryIIIA muta
22	543	84.3	644	18 AAW34816	Novel CryIIIA muta
23	543	84.3	644	18 AAW34817	Novel CryIIIA muta
24	543	84.3	644	18 AAW34818	Novel CryIIIA muta
25	543	84.3	644	18 AAW34819	Novel CryIIIA muta
26	543	84.3	644	18 AAW34820	Novel CryIIIA muta
27	543	84.3	644	18 AAW34821	Novel CryIIIA muta
28	543	84.3	644	18 AAW34822	Novel CryIIIA muta
29	543	84.3	644	18 AAW34823	Novel CryIIIA muta
30	543	84.3	644	18 AAW34824	Novel CryIIIA muta
31	543	84.3	644	18 AAW34825	Novel CryIIIA muta
32	543	84.3	644	18 AAW34826	Novel CryIIIA muta
33	543	84.3	644	18 AAW34827	Novel CryIIIA muta
34	543	84.3	644	18 AAW34828	Novel CryIIIA muta
35	543	84.3	644	18 AAW34829	Novel CryIIIA muta
36	543	84.3	644	18 AAW34830	Novel CryIIIA muta
37	543	84.3	644	18 AAW34831	Novel CryIIIA muta
38	543	84.3	644	18 AAW34832	Novel CryIIIA muta
39	543	84.3	644	18 AAW34833	Novel CryIIIA muta
40	543	84.3	644	18 AAW34834	Novel CryIIIA muta
41	543	84.3	644	18 AAW34835	Novel CryIIIA muta
42	543	84.3	644	18 AAW34836	Novel CryIIIA muta
43	543	84.3	644	18 AAW34837	Novel CryIIIA muta
44	543	84.3	644	18 AAW34838	Novel CryIIIA muta
45	543	84.3	644	18 AAW34839	Novel CryIIIA muta
46	543	84.3	644	18 AAW34840	Novel CryIIIA muta
47	543	84.3	644	18 AAW34841	Novel CryIIIA muta
48	494	76.7	610	16 AAR85782	Blt synthetic (Y2A
49	471	73.1	644	17 AAR99588	Bacillus thuringie
50	453	70.3	644	9 AAP80467	Bacillus thuringie
51	344	53.4	645	18 AAW34784	An artificial modi
52	300	46.6	300	17 AAR99599	B. t. coleopteran
53	271	42.1	914	12 AAR15785	B. thuringiensis to
54	220	34.2	644	22 AAB84195	Amino acid sequenc
55	67	10.4	67	23 AAB81937	Bacillus thuringie
56	67	10.4	80	16 AAR85484	Blt synthetic crys
57	66	10.2	68	16 AAR85483	Blt crystal protei
58	54	8.4	54	23 AAB81938	Bacillus thuringie
59	38	5.9	38	23 AAB81939	Bacillus thuringie
60	36	5.6	36	23 AAB81940	Bacillus thuringie
61	35	5.4	35	23 AAB81941	Bacillus thuringie
62	33	5.1	33	23 AAB81942	Bacillus thuringie
63	31	4.8	31	23 AAB81943	Bacillus thuringie
64	30	4.7	30	23 AAB81944	Bacillus thuringie
65	29	4.7	29	23 AAB81945	Bacillus thuringie
66	28	4.5	28	23 AAB81946	Bacillus thuringie
67	28	4.3	28	23 AAB81947	Bacillus thuringie
68	28	4.3	28	23 AAB81948	Bacillus thuringie
69	28	4.3	28	23 AAB81949	Bacillus thuringie
70	28	4.3	28	23 AAB81950	Bacillus thuringie
71	28	4.3	28	23 AAB81951	Bacillus thuringie
72	27	4.2	27	23 AAB81952	Bacillus thuringie
73	26	4.0	26	23 AAB81953	Bacillus thuringie
74	25	3.9	25	23 AAB81954	Bacillus thuringie
75	25	3.9	25	23 AAB81955	Bacillus thuringie
76	24	3.7	24	23 AAB81956	Bacillus thuringie
77	24	3.7	24	23 AAB81957	Bacillus thuringie
78	24	3.7	24	23 AAB81958	Bacillus thuringie
79	24	3.7	24	23 AAB81959	Bacillus thuringie
80	24	3.7	24	23 AAB81960	Bacillus thuringie
81	24	3.7	24	23 AAB81961	Bacillus thuringie
82	24	3.7	24	23 AAB81962	Bacillus thuringie
83	23	3.6	23	23 AAB81963	Bacillus thuringie

```

84      23      3.6      649      20      AAY23210      Amino acid sequenc
85      21      3.3      21      23      AAU81924      Bacillus thuringie
86      21      3.3      21      23      AAU81924      Bacillus thuringie
87      21      3.3      493      20      AAY23206      Amino acid sequenc
88      21      3.3      572      13      AAR26574      Sequence encoded b
89      21      3.3      651      14      AAR06460      BPGS1208 protoxin
90      21      3.3      651      17      AAR33769      Anticarb 43F. B
91      21      3.3      651      17      AAM06419      Bt isolate pest to
92      21      3.3      651      20      AAY23197      Amino acid sequenc
93      21      3.3      651      20      AAY23200      Amino acid sequenc
94      21      3.3      652      12      AAR14047      B. thuringiensis Cr
95      21      3.3      652      20      AAY23203      Amino acid sequenc
96      21      3.3      652      20      AAY23205      Amino acid sequenc
97      21      3.3      652      20      AAY23207      Amino acid sequenc
98      21      3.3      652      20      AAY23174      Amino acid sequenc
99      21      3.3      652      20      AAY23185      Amino acid sequenc
100     21      3.3      652      20      AAY23186      Amino acid sequenc

```

ALIGNMENTS

RESULT 1
AAP70085 standard; Protein; 644 AA.

AC AAP70085;
DT 04-MAY-1991 (first entry)
DE Sequence of toxin which is toxic to beetles of the order
DE Coleoptera.

KN Microbial pesticide.

OS Bacillus thuringiensis strain san diego.

PN EP213818-A.

PD 11-MAR-1987.

PF 08-AUG-1986; 86EP-0306151.

PR 16-JUN-1986; 86US-0874727.

PR 16-AUG-1985; 85US-0767227.

PA (MYCO-) MYCOGEN CORP.

PI Herrnstadt C, Wilcox E;

DR WPI; 1987-066492/10.

DR N-PSDB; AAN70092.

PT New poly:peptide toxin having pesticidal activity - formed by
PT Bacillus thuringiensis toxin gene, and useful for killing
PT Coleoptera beetles

PS Claim 3; pp15-16; 19pp; English.

CC B. thuringiensis toxin gene toxic to Coleoptera beetles is cloned
CC and expressed. Live micro-organisms for inhibiting the growth of, or
CC killing, the beetles are obtd. The poly:peptide toxin may be isolated
CC for use against the beetles.

XX Sequence 644 AA;

Query Match 100.0%; Score 644; DB 8; Length 644;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDTIKTTENNVEPTNINVOYPLAETPNPTLEDLNYKFFLWMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTTENNVEPTNINVOYPLAETPNPTLEDLNYKFFLWMTADNNTALDSS 60

```

OY      61      TTKDYIOKGISVGDLLGVGFPPGALVSEYTNFLMTIMPSDDPKAMEVOEALMDCK 120
Db      61      TTKDYIOKGISVGDLLGVGFPPGALVSEYTNFLMTIMPSDDPKAMEVOEALMDCK 120
OY      121     IADYAKKKAIAELQGLQNNVEDYVSALSSWQKNPVSSRNHSGRIREFLSQASHFRNS 180
Db      121     IADYAKKKAIAELQGLQNNVEDYVSALSSWQKNPVSSRNHSGRIREFLSQASHFRNS 180
OY      181     MPSEAIAGEYELFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROQLTQEYT 240
Db      181     MPSEAIAGEYELFLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROQLTQEYT 240
OY      241     DHCYKWNVGLDKRGSSYSWVNFNRREBMLTYLDIALPPLDYRLYPREVKTELT 300
Db      241     DHCYKWNVGLDKRGSSYSWVNFNRREBMLTYLDIALPPLDYRLYPREVKTELT 300
OY      301     RDVLTDPFVGNVNLRGYGTFSNENYIRKPHLFDYLRHQFTRPOGYGNDSEFNYS 360
Db      301     RDVLTDPFVGNVNLRGYGTFSNENYIRKPHLFDYLRHQFTRPOGYGNDSEFNYS 360
OY      361     GNVYSTRPSIGSNDIITSPEYGNKSSPEYONLEFNCEKRYRAVANTNLAWPSAVYSGYT 420
Db      361     GNVYSTRPSIGSNDIITSPEYGNKSSPEYONLEFNCEKRYRAVANTNLAWPSAVYSGYT 420
OY      421     KVERSOYNDQTDASTQTYDSKRNVGAVSWDSIDQLPEPTTDDPLEKGYSHQNLVWCEL 480
Db      421     KVERSOYNDQTDASTQTYDSKRNVGAVSWDSIDQLPEPTTDDPLEKGYSHQNLVWCEL 480
OY      481     MGSRGRTIPVLTWTHKSVDFEENMIDSKKITQLPLVAKYKQSGASVYAGPRFTGGDIIOC 540
Db      481     MGSRGRTIPVLTWTHKSVDFEENMIDSKKITQLPLVAKYKQSGASVYAGPRFTGGDIIOC 540
OY      541     TENGSAATIVTPDVVSQKYRARIHVASTQTFFLSLDGAFNORYFDKTIINKGDTLT 600
Db      541     TENGSAATIVTPDVVSQKYRARIHVASTQTFFLSLDGAFNORYFDKTIINKGDTLT 600
OY      601     YNSFNLASFSFPFLSGNNLIQVGTGLSAGDKYVYIDKIEFIPVN 644
Db      601     YNSFNLASFSFPFLSGNNLIQVGTGLSAGDKYVYIDKIEFIPVN 644

```

RESULT 2

AAP82487 standard; protein; 644 AA.

AC AAP82487;

DT 01-NOV-1990 (first entry)

DE Delta endotoxin encoded by cryC.

KN Coleoptera; toxin; cryC; insecticide; delta-endotoxin; Lepidoptera.

OS Bacillus thuringiensis ECG2158.

FT

FT Key Location/Qualifiers

FT Peptide 1..53

FT Protein /label=signal_peptide

FT /note="6 kD"

FT /label-mature_toxin

PN W08808860-A.

PD 17-NOV-1988.

PF 04-MAY-1987; 87WO-US01495.

PR 06-MAY-1987; 87US-0047945.

PA (ECOG-) ECOGEN INC.

PI Donovan WP, Gonzales JM, Levinson BL, Macaluso A;
 XX MPI: 1988-338229/47.
 DR N-PSDB: AAN82139.
 XX
 PT New gene encoding delta endotoxin of *Bacillus thuringiensis* -
 effective as insecticide against Coleoptera.
 XX
 PS Claim 10; Fig 8; 82pp; English.
 XX
 CC The cryC gene encodes a delta endotoxin which is an insecticide
 effective against Coleoptera and Lepidoptera. The sequence was
 isolated from CDNA library, on a plasmid designated pCG212. The
 plasmid can be used to construct an expression vector which can
 be used to transform *B. megaterium* ATCC 35965. Colorado potato
 beetle larvae treated with a suspension of cultured cells were
 dead within one week. The protein can be used as pure crystals
 or in the form of B. t. spores.
 CC See also AAN82141.
 CC
 XX
 SQ Sequence 644 AA;
 XX
 Query Match 100.0%; Score 644; DB 9; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MNPNNRSEHDITKTENNNEVPNNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
 1 MNPNNRSEHDITKTENNNEVPNNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
 61 TTKDVIQKGISVYGDLLGVVGFPGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
 61 TTKDVIQKGISVYGDLLGVVGFPGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
 61 TTKDVIQKGISVYGDLLGVVGFPGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 181 MPFSAISGVEVLEFLTYTAQAANTHFLKDAQIYGEWGEKEDIAEFYKROKLQOEXT 240
 181 MPFSAISGVEVLEFLTYTAQAANTHFLKDAQIYGEWGEKEDIAEFYKROKLQOEXT 240
 181 MPFSAISGVEVLEFLTYTAQAANTHFLKDAQIYGEWGEKEDIAEFYKROKLQOEXT 240
 241 DHCYKMNNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPFLYDVRLPYKREVTTELT 300
 241 DHCYKMNNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPFLYDVRLPYKREVTTELT 300
 241 DHCYKMNNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPFLYDVRLPYKREVTTELT 300
 241 DHCYKMNNGLDKLRGSSYSWVNFNRYRREMTLVLDLALPFLYDVRLPYKREVTTELT 300
 301 RDVLTDPYGVNMLRGYGTTFSENIENYIRKPHLFDYLRHQFTFRQPGYGGDSFNYS 360
 301 RDVLTDPYGVNMLRGYGTTFSENIENYIRKPHLFDYLRHQFTFRQPGYGGDSFNYS 360
 301 RDVLTDPYGVNMLRGYGTTFSENIENYIRKPHLFDYLRHQFTFRQPGYGGDSFNYS 360
 301 RDVLTDPYGVNMLRGYGTTFSENIENYIRKPHLFDYLRHQFTFRQPGYGGDSFNYS 360
 361 GNVYSTPSTSGSNDITSPRYGKSSRPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 361 GNVYSTPSTSGSNDITSPRYGKSSRPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 361 GNVYSTPSTSGSNDITSPRYGKSSRPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 361 GNVYSTPSTSGSNDITSPRYGKSSRPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
 421 KVEFSQYNDQDEASTQTYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOINYYWCF 480
 421 KVEFSQYNDQDEASTQTYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOINYYWCF 480
 421 KVEFSQYNDQDEASTQTYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOINYYWCF 480
 421 KVEFSQYNDQDEASTQTYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHOINYYWCF 480
 481 MGSRGRTIPVLTWTHKSVDFPNMIDSKITQLPLVKAAYKQSGSVVAGRGFGDITIC 540
 481 MGSRGRTIPVLTWTHKSVDFPNMIDSKITQLPLVKAAYKQSGSVVAGRGFGDITIC 540
 481 MGSRGRTIPVLTWTHKSVDFPNMIDSKITQLPLVKAAYKQSGSVVAGRGFGDITIC 540
 481 MGSRGRTIPVLTWTHKSVDFPNMIDSKITQLPLVKAAYKQSGSVVAGRGFGDITIC 540
 541 TENSSAATITVTPPVSYSOXKRAHIAHASTSOITFTSLDGAPENOYFPTKINKGDTLT 600
 541 TENSSAATITVTPPVSYSOXKRAHIAHASTSOITFTSLDGAPENOYFPTKINKGDTLT 600
 541 TENSSAATITVTPPVSYSOXKRAHIAHASTSOITFTSLDGAPENOYFPTKINKGDTLT 600
 541 TENSSAATITVTPPVSYSOXKRAHIAHASTSOITFTSLDGAPENOYFPTKINKGDTLT 600
 601 YNSFNLASFTPFELSGNNLQIGVTGLSAGDKYVIDKIEEIPVN 644
 601 YNSFNLASFTPFELSGNNLQIGVTGLSAGDKYVIDKIEEIPVN 644
 601 YNSFNLASFTPFELSGNNLQIGVTGLSAGDKYVIDKIEEIPVN 644
 601 YNSFNLASFTPFELSGNNLQIGVTGLSAGDKYVIDKIEEIPVN 644
 RESULT 3
 AAP94679

ID AAP94679 standard; protein; 644 AA.
 XX
 AC AAP94679;
 XX
 DT 17-JUL-1990 (first entry)
 DT
 XX
 DE Amino acid sequence of the Btl3 protein.
 XX
 KW *Bacillus thuringiensis* tenebrionis; 66 kDa crystal protein; btl3 gene;
 KW Btl3 protein; toxin; Coleoptera; p1VE38.
 XX
 OS *Bacillus thuringiensis*.
 XX
 FH Key Location/Qualifiers
 FT Region 58..79
 FT /note="N-terminal residues of the Btl3 protein"
 FT Misc-difference 58
 FT /note="This residue was not unambiguously determined.
 FT It could possibly be Ser."
 FT Misc-difference 60
 FT /note="As above. It could possibly be Pro."
 FT Misc-difference 64
 FT /note="As above. It could possibly be Gln."
 FT
 XX W08901515-A.
 PD 23-FEB-1989.
 XX
 PF 15-AUG-1988; 88WO-EP00752.
 XX
 PR 29-DEC-1987; 87GB-0030261.
 XX
 PA (PLAN-) PLANT GENETIC SYSTEMS.
 XX
 PI Vaeck M, Hofte H, Botterman J;
 XX
 DR MPI: 1989-068871/09.
 DR N-PSDB: AAN91071.
 XX
 PT Plant cell transformed with DNA -
 PT is for *Bacillus thuringiensis* toxic protein and is resistant to
 PT Coleoptera pests
 PS Disclosure: ; 35pp; English.
 XX
 CC The btl3 gene encodes a 66 kDa crystal protein (the Btl3 protein) which
 is believed to be the active protein in the crystal toxin (the Btl3
 toxin) produced by *Bacillus thuringiensis* (B.t.) tenebrionis and B.t.
 CC 51. The patent is for a transformed plant cell which includes inserted
 CC in its genome, the btl3 gene, or a fragment which encodes the 66kD
 CC crystal protein. Plant cells contg. DNA encoding this protein are
 CC protected against Coleoptera. Also new are plants (and their seeds)
 CC contg. these cells; a specific DNA sequence of 1760 b; the crystal
 CC protein; and microorganisms transformed with the DNA.
 CC
 XX
 SQ Sequence 644 AA;
 XX
 Query Match 100.0%; Score 644; DB 10; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MNPNNRSEHDITKTENNNEVPNNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
 1 MNPNNRSEHDITKTENNNEVPNNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
 61 TTKDVIQKGISVYGDLLGVVGFPGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
 61 TTKDVIQKGISVYGDLLGVVGFPGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
 61 TTKDVIQKGISVYGDLLGVVGFPGALVSFTYNTFLNTIMPSEDPKAKMEQVEALMDOK 120
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180
 121 IADYANKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHFRNS 180

```

OY 181 MSPAISGEVLEFLTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
DB 181 MSPAISGEVLEFLTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
OY 241 DHCVKMYNNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLYDVRLYPREKVTTEL 300
DB 241 DHCVKMYNNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLYDVRLYPREKVTTEL 300
OY 301 RDVLTDPPIGVNNLRGTYGTFPSNIENYIRKPHLFDYLRHQHTRPQPGYNDSPFNWS 360
DB 301 RDVLTDPPIGVNNLRGTYGTFPSNIENYIRKPHLFDYLRHQHTRPQPGYNDSPFNWS 360
OY 361 GNVYSTRPSIGSNDIITSPFYGNKSEPEVONLEFNGEKYRAVANTNLAVMPSAVYSGVT 420
DB 361 GNVYSTRPSIGSNDIITSPFYGNKSEPEVONLEFNGEKYRAVANTNLAVMPSAVYSGVT 420
OY 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
DB 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
OY 481 MOGSRGTIPVLMTWTHKSVDFENMIDSKKITQPLVKAAYKLOGSASVAGPRTGGDIIOC 540
DB 481 MOGSRGTIPVLMTWTHKSVDFENMIDSKKITQPLVKAAYKLOGSASVAGPRTGGDIIOC 540
OY 541 TENGSAAATYYTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
DB 541 TENGSAAATYYTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
OY 601 YNSFNLASFSSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

```

RESULT 4
AAP95585
AAP95585 standard; protein: 644 AA.

```

AC AAP95585;
DB 08-AUG-1990 (first entry)
DE M-7 crystal toxin.
KW M-7 toxin crystal; Coleoptera; beetle.
OS Bacillus thuringiensis strain san-diego (NRRL B-15939).
PN US4853331-A.
PD 01-AUG-1989.
PE 30-NOV-1988; 88US-0278292.
PR 15-AUG-1985; 85US-0767227.
PR 15-JUL-1988; 88US-0219420.
PA (MTCO-) MYCOGEN CORP.
PI Hernstadt C, Wilcox E;
PI WPI; 1989-277854/38.
DR N-PSDB; AAN90957.
XX
XX
XX Cloning of Bacillus thuringiensis toxin gene -
XX for expression of protein toxic to beetles of order Coleoptera.
XX Disclosure; Page 13-14; 10pp; English.
XX
XX The gene encoding the toxin can be cloned and used to produce the
XX M-7 crystal which has activity against eg western spotted cucumber
XX beetle, and northern, western and southern corn rootworm.
XX
XX Sequence 644 AA;
SQ

```

```

Query Match 100.0%; Score 644; DB 10; Length 644;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNPNSRSHDITKTENNEVPTNHYOYPLAETPPTLEDLYKFEFLMTADNNTALDSS 60
DB 1 MNPNSRSHDITKTENNEVPTNHYOYPLAETPPTLEDLYKFEFLMTADNNTALDSS 60
OY 61 TTKDVIQKISVVDLLGVVGFPEFGALVSEFYTFNLTIMPSEDPKMAFEQYEAALMDOK 120
DB 61 TTKDVIQKISVVDLLGVVGFPEFGALVSEFYTFNLTIMPSEDPKMAFEQYEAALMDOK 120
OY 121 IADYAKKALAELOGLONNVEDYVLSLSQKNVDVSRNPHSGRIRELSQAESHFRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVLSLSQKNVDVSRNPHSGRIRELSQAESHFRNS 180
OY 181 MSPAISGEVLEFLTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
DB 181 MSPAISGEVLEFLTTAAQANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQOET 240
OY 241 DHCVKMYNNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLYDVRLYPREKVTTEL 300
DB 241 DHCVKMYNNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLYDVRLYPREKVTTEL 300
OY 301 RDVLTDPPIGVNNLRGTYGTFPSNIENYIRKPHLFDYLRHQHTRPQPGYNDSPFNWS 360
DB 301 RDVLTDPPIGVNNLRGTYGTFPSNIENYIRKPHLFDYLRHQHTRPQPGYNDSPFNWS 360
OY 361 GNVYSTRPSIGSNDIITSPFYGNKSEPEVONLEFNGEKYRAVANTNLAVMPSAVYSGVT 420
DB 361 GNVYSTRPSIGSNDIITSPFYGNKSEPEVONLEFNGEKYRAVANTNLAVMPSAVYSGVT 420
OY 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
DB 421 KVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEKGYSHOANTVMCFL 480
OY 481 MOGSRGTIPVLMTWTHKSVDFENMIDSKKITQPLVKAAYKLOGSASVAGPRTGGDIIOC 540
DB 481 MOGSRGTIPVLMTWTHKSVDFENMIDSKKITQPLVKAAYKLOGSASVAGPRTGGDIIOC 540
OY 541 TENGSAAATYYTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
DB 541 TENGSAAATYYTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFEDKTINKGDTLT 600
OY 601 YNSFNLASFSSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFSSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

```

RESULT 5
AAR39751
AAR39751 standard; protein: 644 AA.
AC AAR39751;
DB 28-JAN-1994 (first entry)
DE Delta endotoxin.
KW Endotoxin; Bacillus; lice; insecticide; sheep.
OS Bacillus thuringiensis PS40D1.
PN W09314641-A.
PD 05-AUG-1993.
PE 31-DEC-1992; 92MO-US11337.
PR 29-JAN-1992; 92US-0828768.
XX
XX (MTCO) MYCOGEN CORP.

```

XX Hickie LA, Payne J;
PI
XX
XX WPI: 1993-258266/32.
DR
XX N-PSDB: AAQ47288.
XX
PT Controlling biting lice on sheep - comprises administering
PT Bacillus thuringiensis toxins to host
PS
XX Disclosure: Page 31-32; 64pp; English.
XX
CC Many strains of Bacillus thuringiensis (B.t.) produce insecticidal
CC delta endotoxins. A number of these endotoxins have been found to
CC be toxic to Damillina ovis, the biting louse of sheep. The B.T.
CC isolates which produce these toxins can be grown and the delta
CC endotoxin which is produced can be recovered by standard procedures.
CC The genes encoding these endotoxins can also be transferred to a
CC suitable host via a recombinant vector and the resulting
CC transformants used in methods to control lice.
XX
SQ Sequence 644 AA:
Query Match 100.0%; Score 644; DB 14; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
DB 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
QY 61 TTKDVYOKGISVVGDLGVVGFPGGALVSFTNTLNTWPSDEDPKAFMEVEALMDOK 120
DB 61 TTKDVYOKGISVVGDLGVVGFPGGALVSFTNTLNTWPSDEDPKAFMEVEALMDOK 120
QY 121 IDVYAKNKALAELOGQNNVEDYVSALSSWQKNPVSSRRPHSGGRIRLEFSQAESHFNS 180
DB 121 IDVYAKNKALAELOGQNNVEDYVSALSSWQKNPVSSRRPHSGGRIRLEFSQAESHFNS 180
QY 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKROKLQOEXT 240
DB 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKROKLQOEXT 240
QY 241 DHCVKWYNGDLKRGSSYESWVNFRRREMTLVLDIALFPLVDRLVLPKEVKTTELT 300
DB 241 DHCVKWYNGDLKRGSSYESWVNFRRREMTLVLDIALFPLVDRLVLPKEVKTTELT 300
QY 301 RDVLTDPYGVNMLRGYGTTFNSIENYIRKPHLFYDLHRIQFHTRPQGYGNDSEFNWS 360
DB 301 RDVLTDPYGVNMLRGYGTTFNSIENYIRKPHLFYDLHRIQFHTRPQGYGNDSEFNWS 360
QY 361 GNVVSTRPSIGSNDITSPFYGKSSSPVONLEFNGEKYRAVANNTLAWPFAVYSGVT 420
DB 361 GNVVSTRPSIGSNDITSPFYGKSSSPVONLEFNGEKYRAVANNTLAWPFAVYSGVT 420
QY 421 KVEFSQYNDQTDASTQYDSKRNVCASWDSIDQLPETTDEPLEKGYSHQNLVWCF 480
DB 421 KVEFSQYNDQTDASTQYDSKRNVCASWDSIDQLPETTDEPLEKGYSHQNLVWCF 480
QY 481 MGSRGCTPVLTWTHKSVDFENMIDSKKITQLPLVKAYLQSGASVAVAGFRFGDIIOC 540
DB 481 MGSRGCTPVLTWTHKSVDFENMIDSKKITQLPLVKAYLQSGASVAVAGFRFGDIIOC 540
QY 541 TENGSATITVTPPVVSQYRARIHASNISQITFTLSLGGAFPNQYFPFKTINKGDTLT 600
DB 541 TENGSATITVTPPVVSQYRARIHASNISQITFTLSLGGAFPNQYFPFKTINKGDTLT 600
QY 601 YNSFNLASFTPELISGNMLQIGVGLSAGDKYVIDKIEEIPVN 644
DB 601 YNSFNLASFTPELISGNMLQIGVGLSAGDKYVIDKIEEIPVN 644
RESULT 6
AAR56697

```

```

ID AAR56697 standard; Protein: 644 AA.
XX
XX AAR56697:
AC
XX
XX 27-MAR-1995 (first entry)
DT
XX
XX CryIIA insecticidal crystal protein.
DE
XX
XX CryIIA: CryIIIA; CryIIB; CryC; P-2; CryBI: insecticidal protein crystal.
KW
XX Lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
KW probe; hybridisation.
XX
XX Bacillus thuringiensis.
XX
XX US338544-A.
XX
XX 16-AUG-1994.
XX
XX 16-APR-1987; 87US-0039542.
XX
XX 16-APR-1987; 87US-0039542.
XX
XX 11-JUL-1989; 89US-0379015.
XX
XX 28-AUG-1991; 91US-0751452.
XX
XX 26-FEB-1993; 93US-0023736.
XX
XX (ECOG-) ECOGEN INC.
XX
XX Donovan WP;
PI
XX
XX WPI: 1994-263236/32.
DR
XX N-PSDB: AAQ71026.
XX
XX New Cry IIB protein - obtd. from the cry II B gene in Bacillus
XX thuringiensis var. Kurstaki, active against lepidopteran insects
XX
XX Example 7; Fig 4A-4D; 39pp; English.
XX
XX This sequence shows the amino acid sequence of CryIIIA protein. The
XX promoter from the CryIIIA gene sequence was fused to the protein
XX coding region of the CryBI gene (AAQ71027). The recombinant hybrid
XX fusion gene expressed the CryBI crystal protein more efficiently
XX than its native promoter. CryIIB encodes an insecticidal crystal
XX protein isolated from Bacillus thuringiensis var. kurstaki. It
XX produces crystal proteins during sporulation which are specifically
XX toxic to certain orders and species of insects, esp. lepidopterans.
XX CryIIB can be used in compositions used as environmentally acceptable
XX insecticides. (See also AAR56696 and AAR56698)
XX
XX
SQ Sequence 644 AA:
Query Match 100.0%; Score 644; DB 15; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
DB 1 MNPNNSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNTKEFLKMTADNNTALDSS 60
QY 61 TTKDVYOKGISVVGDLGVVGFPGGALVSFTNTLNTWPSDEDPKAFMEVEALMDOK 120
DB 61 TTKDVYOKGISVVGDLGVVGFPGGALVSFTNTLNTWPSDEDPKAFMEVEALMDOK 120
QY 121 IDVYAKNKALAELOGQNNVEDYVSALSSWQKNPVSSRRPHSGGRIRLEFSQAESHFNS 180
DB 121 IDVYAKNKALAELOGQNNVEDYVSALSSWQKNPVSSRRPHSGGRIRLEFSQAESHFNS 180
QY 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKROKLQOEXT 240
DB 181 MPFALISGEVLEFLTTYAAQANTHFLKDAQIYGEWGEKEDIAEFKROKLQOEXT 240
QY 241 DHCVKWYNGDLKRGSSYESWVNFRRREMTLVLDIALFPLVDRLVLPKEVKTTELT 300
DB 241 DHCVKWYNGDLKRGSSYESWVNFRRREMTLVLDIALFPLVDRLVLPKEVKTTELT 300

```

QY 301 RDVLTDPVGVNLRGVTTFSENIENYIRKPHLFDYLRHIOFHTRRPOGYSNDSPNYS 360
 CC 301 RDVLTDPVGVNLRGVTTFSENIENYIRKPHLFDYLRHIOFHTRRPOGYSNDSPNYS 360
 CC 301 RDVLTDPVGVNLRGVTTFSENIENYIRKPHLFDYLRHIOFHTRRPOGYSNDSPNYS 360
 Db 301 RDVLTDPVGVNLRGVTTFSENIENYIRKPHLFDYLRHIOFHTRRPOGYSNDSPNYS 360
 QY 361 GNVYSTRPSIGSNDITTSPEYGNKSSPEVONLEFNGEKYRAVANINLAWPSSAVYSGVT 420
 Db 361 GNVYSTRPSIGSNDITTSPEYGNKSSPEVONLEFNGEKYRAVANINLAWPSSAVYSGVT 420
 QY 421 KVEFSQYNDOTDEASTQYTDKSRNKGAVSWDSIDQLPETTDEPLEKGYSHOINVMCFL 480
 Db 421 KVEFSQYNDOTDEASTQYTDKSRNKGAVSWDSIDQLPETTDEPLEKGYSHOINVMCFL 480
 QY 481 MGSRGITPVLWTNHSVDFEPMNIDSKKITQPLVKAAYLQSGASVAGPRTGGDIIOC 540
 Db 481 MGSRGITPVLWTNHSVDFEPMNIDSKKITQPLVKAAYLQSGASVAGPRTGGDIIOC 540
 QY 541 TENGSAATITVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFDDKTINKGDTLT 600
 Db 541 TENGSAATITVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFDDKTINKGDTLT 600
 QY 601 YNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Db 601 YNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 7
 AAR56698
 ID AAR56698 standard; Protein: 644 AA.

AC AAR56698;

DT 27-MAR-1995 (first entry)

DE CryiIB insecticidal crystal protein.

KW CryiIA, CryiIIA, CryiIB, Cryc, P-2; CryBI; insecticidal protein crystal;
 lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;
 probe; hybridisation.

OS Bacillus thuringiensis.

XX US5338544-A.

PD 16-AUG-1994.

XX 16-APR-1987; 87US-0039542.

PR 16-APR-1987; 87US-0039542.

PR 11-JUL-1989; 89US-0379015.

PR 28-AUG-1991; 91US-0751452.

PR 26-FEB-1993; 93US-0023736.

XX (ECOCG-) ECOGEN INC.

XX DONOVAN WP;

XX WPI; 1994-263236/32.

DR N-PSDB; AAQ71027.

XX New Cry IIB protein - obt'd. from the cry II B gene in Bacillus

XX thuringiensis var. kurstaki, active against lepidopteran insects

XX Claim 1; Fig 6A-6D; 39pp; English.

CC This sequence shows the amino acid sequence of CryiIB protein. The
 CC promoter from the CryiIA gene (AAQ71026) sequence was fused to the
 CC protein coding region of the CryiIB gene. The recombinant hybrid
 CC fusion gene expressed the CryiIB crystal protein more efficiently
 CC than its native promoter. CryiIB encodes an insecticidal crystal
 CC protein isolated from Bacillus thuringiensis var. kurstaki. It
 CC produces crystal proteins during sporulation which are specifically
 CC toxic to certain orders and species of insects, esp. lepidopterans.

CC CryiIB can be used in compositions used as environmentally acceptable
 CC insecticides. (See also AAR56696 and AAR56698)

SO Sequence 644 AA;

Query Match 100.0%; Score 644; DB 15; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNENVEPTNHVQYPLAETPPTLEDINKEEFLBMTADNNTALDSS 60

Db 1 MNPNNRSEHDITKTENNENVEPTNHVQYPLAETPPTLEDINKEEFLBMTADNNTALDSS 60

QY 61 TTKDVYQKGISVVDLLGVGFPFGALVSEFYTNFLTMTIPSEDDPKAFMEQVBAIMDQK 120

Db 61 TTKDVYQKGISVVDLLGVGFPFGALVSEFYTNFLTMTIPSEDDPKAFMEQVBAIMDQK 120

QY 121 IADYAKNKALAELOGLONNVEDYVSSALSMOKNPVSSRNPHSGRTRELFSQASHFRNS 180

Db 121 IADYAKNKALAELOGLONNVEDYVSSALSMOKNPVSSRNPHSGRTRELFSQASHFRNS 180

QY 181 MPSEFAISGEYVFLTTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLQKLTQEVY 240

Db 181 MPSEFAISGEYVFLTTTAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLQKLTQEVY 240

QY 241 DHCYKMYNGLDKLRGSSYSESWNFNRYRREMTLTVLDLALPPLVDVRYPREVTELT 300

Db 241 DHCYKMYNGLDKLRGSSYSESWNFNRYRREMTLTVLDLALPPLVDVRYPREVTELT 300

QY 301 RDVLTDPVGVNLRGVTTFSENIENYIRKPHLFDYLRHIOFHTRRPOGYSNDSPNYS 360

Db 301 RDVLTDPVGVNLRGVTTFSENIENYIRKPHLFDYLRHIOFHTRRPOGYSNDSPNYS 360

QY 361 GNVYSTRPSIGSNDITTSPEYGNKSSPEVONLEFNGEKYRAVANINLAWPSSAVYSGVT 420

Db 361 GNVYSTRPSIGSNDITTSPEYGNKSSPEVONLEFNGEKYRAVANINLAWPSSAVYSGVT 420

QY 421 KVEFSQYNDOTDEASTQYTDKSRNKGAVSWDSIDQLPETTDEPLEKGYSHOINVMCFL 480

Db 421 KVEFSQYNDOTDEASTQYTDKSRNKGAVSWDSIDQLPETTDEPLEKGYSHOINVMCFL 480

QY 481 MGSRGITPVLWTNHSVDFEPMNIDSKKITQPLVKAAYLQSGASVAGPRTGGDIIOC 540

Db 481 MGSRGITPVLWTNHSVDFEPMNIDSKKITQPLVKAAYLQSGASVAGPRTGGDIIOC 540

QY 541 TENGSAATITVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFDDKTINKGDTLT 600

Db 541 TENGSAATITVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFDDKTINKGDTLT 600

QY 601 YNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 644

Db 601 YNSFNLASFTPELSEGNMLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 8
 AAY23214
 ID AAY23214 standard; Protein: 652 AA.

XX AAY23214;

AC AAY23214;

DT 24-AUG-1999 (first entry)

XX Amino acid sequence of Cry3A protein.

XX Cry3Bb; mutant; insecticidal activity; insecticidal specificity;

XX Coleoptera; southern corn rootworm; western corn root worm; Cry3A;

XX Diabrotica undecimpunctata howardi Barber; transgenic plant;

XX Diabrotica virgifera virgifera Leconte; insecticide resistance.

OS Bacillus thuringiensis.

XX W09931248-A1.

PD 24-JUN-1999.
 XX 17-DEC-1998; 98WO-US#6852.
 XX 18-DEC-1997; 97US-0996441.
 PR 18-DEC-1997; 97US-0993170.
 PR 18-DEC-1997; 97US-0993722.
 PR 18-DEC-1997; 97US-0993775.
 XX (ECOG-) ECOGEN INC.
 PA (MONS) MONSANTO CO.
 XX Brusson SM, Bryson JW, English L, Kulesza CA, Malvar TM,
 PI Romano C, Slatkin SL, Von Tersch MA, Walters FS;
 XX WPI: 1999-395184/33.
 DR
 XX
 XX
 PT Insecticidal *Bacillus thuringiensis* proteins
 XX
 PS Disclosure: Page 505-507; 512pp; English.
 XX The present sequence represents the Cry3A protein. The specification
 CC describes new *Bacillus thuringiensis* Cry3Bb mutant proteins, and
 CC provides methods for producing them. The B. thuringiensis Cry3Bb
 CC polypeptide was modified to have improved insecticidal activity or
 CC enhanced insecticidal specificity against a target insect. The
 CC modification comprises at least one amino acid substitution, addition,
 CC or deletion in the primary sequence of the native or unmodified Cry3Bb
 CC polypeptide, wherein the substitution or deletion occurs at a position
 CC corresponding to from about amino acids 1-365 of the unmodified
 CC polypeptide sequence (AAV23207 represents the wild type Cry3Bb
 CC protein). The polypeptide can be used to kill coleopteran pests,
 CC especially by application to the environment. It is especially
 CC useful against southern corn rootworm and western corn root worm,
 CC (*Diabrotica undecimpunctata howardi* Barber, and *Diabrotica virgifera*
 CC *vergifera* Lecoute respectively). The mutant cry3Bb polynucleotides
 CC can also be used to produce transgenic plants with increased
 CC insecticide resistance.
 CC
 XX
 XX
 SQ Sequence 652 AA:
 Query Match 100.0%; Score 644; DB 20; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 KVERSOYNDOTDEASTOTYDSCRNVGAVSWDSIDOLPPEITDDELEKGYSHQNTVMCEFL 480
 |||||||
 DB 429 KVERSOYNDOTDEASTOTYDSCRNVGAVSWDSIDOLPPEITDDELEKGYSHQNTVMCEFL 488
 OY 481 MOGSRGTIPVLTWTHKSVDFEPMIDSKKITQPLVAKYKQSGASVAVGPRFTGDIIOC 540
 |||||||
 DB 489 MOGSRGTIPVLTWTHKSVDFEPMIDSKKITQPLVAKYKQSGASVAVGPRFTGDIIOC 548
 OY 541 TENGAATITVTPDVSTSQKRRARIRHASTQITFTLSLDGAFPNQYFPDKTINKGDTLT 600
 |||||||
 DB 549 TENGAATITVTPDVSTSQKRRARIRHASTQITFTLSLDGAFPNQYFPDKTINKGDTLT 608
 OY 601 YNSFNLASFPNPELSCNNLOIGVTLGASGDKYIDKIEFTIPVN 644
 |||||||
 DB 609 YNSFNLASFPNPELSCNNLOIGVTLGASGDKYIDKIEFTIPVN 652

RESULT 9
 AAM00334
 ID AAM00334 standard; Protein: 597 AA.
 XX
 AC AAM00334;
 XX
 DT 02-JAN-1997 (first entry)
 XX
 DE *Bacillus thuringiensis* pesticidal protein toxin (native).
 XX
 KW *Bacillus thuringiensis*; plant; codon; crystal protein; Bt gene;
 XX toxin; insect; pest; tobacco hornworm.
 OS *Bacillus thuringiensis*.
 XX
 PN US5567600-A.
 PD
 XX 22-OCT-1996.
 PF
 XX 24-SEP-1983; 83US-0535354.
 PR 06-JAN-1995; 95US-0369835.
 PR 24-SEP-1983; 83US-0535354.
 PR 04-APR-1986; 86US-0848733.
 PR 09-SEP-1988; 88US-0242482.
 PR 28-JAN-1992; 92US-0827844.
 PR 03-MAY-1993; 93US-0057191.
 XX
 XX (MTCO) MYCOGEN PLANT SCI INC.
 PA
 PI Adang MJ, Merlo DJ, Murray EE, Rochelleau JA;
 XX
 DR WPI: 1996-484994/48.
 DR N-FSDB: AAT40341.
 PT
 PT Increasing *Bacillus thuringiensis* gene expression in plants - by
 reducing frequency of codon usages that are rare in plants
 PS
 PS Disclosure: Fig 1; 23pp; English.
 XX
 XX The synthetic Bt gene sequence (AAT40340) differs from the native
 CC sequence as found in p344pst-Met5 (AAT40341). Changes in amino acids
 CC occur in the synthetic sequence with alanine replacing threonine at
 CC residue 2 and leucine replacing the stop at residue 596 followed by
 CC the addition of 13 amino acids at the C-terminus.
 CC At least 32% of the codons and/or at least 11% of the nucleotides
 CC in the coding sequence of the native Bt gene are changed.
 CC By avoiding codon usage that are rare in plants, plants that have
 CC more Bt crystal protein than plants contg. the native Bt gene, and
 CC are thus more toxic to insect pests such as tobacco hornworm, can be
 CC produced.
 XX
 SQ Sequence 597 AA;
 Query Match 92.7%; Score 597; DB 17; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 597: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALDSSTTKDVIOKGISVGDLLGVGFPFGALVSFYTNFLTWTWPSDEPK 107
 DB 1 MTADNNTALDSSTTKDVIOKGISVGDLLGVGFPFGALVSFYTNFLTWTWPSDEPK 60
 QY 108 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSSQKNPVSRRNHSQGRIR 167
 DB 61 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSSQKNPVSRRNHSQGRIR 120
 QY 168 ELFSQAESHRNMPSPFALSISGEVFLTTYAQAANTHLFLKDAQIYGEEMGEKEDIAD 227
 DB 121 ELFSQAESHRNMPSPFALSISGEVFLTTYAQAANTHLFLKDAQIYGEEMGEKEDIAD 180
 QY 228 FYKROLKLTQOXYTHDCVKKNVNGDLKRGSSYESVWNFNRYRREMTLVLDLALFPLYD 287
 DB 181 FYKROLKLTQOXYTHDCVKKNVNGDLKRGSSYESVWNFNRYRREMTLVLDLALFPLYD 240
 QY 288 VRLYPEVKTLETRDVLDPDPIVGNVNLKRGYGTFSNIENYIRKPHLFDYLHRIQFHTRQ 347
 DB 241 VRLYPEVKTLETRDVLDPDPIVGNVNLKRGYGTFSNIENYIRKPHLFDYLHRIQFHTRQ 300
 QY 348 PGYGGNDSFNWYSGNVSTRPSIGSNDIITSPFYGNKSSPVONLEFNGEKYRAVANTN 407
 DB 301 PGYGGNDSFNWYSGNVSTRPSIGSNDIITSPFYGNKSSPVONLEFNGEKYRAVANTN 360
 QY 408 LAWPSAVYSGVTKVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 467
 DB 361 LAWPSAVYSGVTKVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 420
 QY 468 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKITQLPLVAKYKLOGASVY 527
 DB 421 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKITQLPLVAKYKLOGASVY 480
 QY 528 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITPTLSLDGAPFNQY 587
 DB 481 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITPTLSLDGAPFNQY 540
 QY 588 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
 DB 541 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 597

RESULT 10
 AAY69666
 ID AAY69666 standard; Protein: 597 AA.
 AC AAY69666;
 XX 08-MAY-2000 (first entry)
 DT 08-MAY-2000 (first entry)
 DE Wild-type *Bacillus thuringiensis* (Bt) toxin.
 XX Bt toxin; codon usage; expression; transgenic plant; pesticide;
 KW insecticide.
 XX *Bacillus thuringiensis* var. *tenebrionis*.
 OS *Bacillus thuringiensis* var. *tenebrionis*.
 PN US6015891-A.
 XX 18-JAN-2000.
 PD 18-JAN-2000.
 XX 29-AUG-1996; 96US-0705438.
 PF 29-AUG-1996; 96US-0705438.
 XX 06-JAN-1995; 95US-0369835.
 PR 09-SEP-1988; 88US-0242482.
 PR 28-JAN-1992; 92US-0827844.
 PR 03-MAY-1993; 93US-0057191.
 XX (MYCO) MYCOGEN PLANT SCI INC.
 PA Murray EE, Adang MJ;
 PI
 XX

DR WPI: 2000-136460/12.
 DR N-PSDB; AA259993.
 XX Synthetic *Bacillus thuringiensis* pesticidal toxin gene for expression
 PT in plant cells has coding sequence adapted to codon usage bias of
 PT plants -
 XX
 PS Example 3; Columns 31-36; 29pp; English.
 XX
 CC The invention relates to a novel synthetic *Bacillus thuringiensis* (Bt)
 CC toxin gene (AA259994) which is expressed at a high level in descendant
 CC plant cells and encodes a pesticidal protein toxin. The synthetic gene
 CC was designed to be expressed in plants at a higher level than wild-type
 CC Bt genes (e.g., AA259993). This was accomplished by altering the DNA
 CC sequence of the native Bt gene such that it contained codons
 CC preferred by highly expressed plant genes, had an A+T content comparable
 CC to that found in plant genes and contained a plant initiation sequence.
 CC Additionally, sequences that cause destabilization, inappropriate
 CC polyadenylation, degradation and termination of RNA were eliminated,
 CC and sequences that constitute RNA hairpin and splice sites were avoided.
 CC The resulting synthetic Bt gene has at least 10% of its nucleotides
 CC altered as compared with the native Bt gene. The synthetic Bt gene is
 CC operably linked to a plant-expressible promoter and can be transformed
 CC into plant cells. The gene is used to produce transgenic plants having
 CC resistance to pests, particularly insects. The modifications produced in
 CC the coding sequence increases the level of expression of Bt toxin in
 CC plants. The present sequence represents wild-type *Bacillus thuringiensis*
 CC (var. *tenebrionis*, Btc) Bt toxin.
 CC
 XX Sequence 597 AA:
 SQ
 Query Match 92.7%; Score 597; DB 21; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALDSSTTKDVIOKGISVGDLLGVGFPFGALVSFYTNFLTWTWPSDEPK 107
 DB 1 MTADNNTALDSSTTKDVIOKGISVGDLLGVGFPFGALVSFYTNFLTWTWPSDEPK 60
 QY 108 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSSQKNPVSRRNHSQGRIR 167
 DB 61 AFMEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSSQKNPVSRRNHSQGRIR 120
 QY 168 ELFSQAESHRNMPSPFALSISGEVFLTTYAQAANTHLFLKDAQIYGEEMGEKEDIAD 227
 DB 121 ELFSQAESHRNMPSPFALSISGEVFLTTYAQAANTHLFLKDAQIYGEEMGEKEDIAD 180
 QY 228 FYKROLKLTQOXYTHDCVKKNVNGDLKRGSSYESVWNFNRYRREMTLVLDLALFPLYD 287
 DB 181 FYKROLKLTQOXYTHDCVKKNVNGDLKRGSSYESVWNFNRYRREMTLVLDLALFPLYD 240
 QY 288 VRLYPEVKTLETRDVLDPDPIVGNVNLKRGYGTFSNIENYIRKPHLFDYLHRIQFHTRQ 347
 DB 241 VRLYPEVKTLETRDVLDPDPIVGNVNLKRGYGTFSNIENYIRKPHLFDYLHRIQFHTRQ 300
 QY 348 PGYGGNDSFNWYSGNVSTRPSIGSNDIITSPFYGNKSSPVONLEFNGEKYRAVANTN 407
 DB 301 PGYGGNDSFNWYSGNVSTRPSIGSNDIITSPFYGNKSSPVONLEFNGEKYRAVANTN 360
 QY 408 LAWPSAVYSGVTKVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 467
 DB 361 LAWPSAVYSGVTKVEFSQYNDQTDASTQYDYSKRNKAVSWDSIDQLPETTDEPLEK 420
 QY 468 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKITQLPLVAKYKLOGASVY 527
 DB 421 GYSHOLNVMCFMLOGSRGTIPVLTWTHKSVDFFNMIDSKITQLPLVAKYKLOGASVY 480
 QY 528 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITPTLSLDGAPFNQY 587
 DB 481 AGPRFTGGDIIOCTENGSAATITVTPDVYSQYRARIHYASTQITPTLSLDGAPFNQY 540
 QY 588 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
 DB 541 YEDKTIKNGDITLYNSFNLASFPFELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 597

Db 541 YFDKTKGDTLTYNSFNLASFSTPELISGNLQIGVTGLSAGDKVYIDKIEFIPVN 597

RESULT 11

AA05537 standard; protein: 610 AA.

AA05537:

02-AUG-1990 (first entry)

Synthetic Bacillus thuringiensis toxin.

Btl: toxin; insecticide; crystal protein.

Synthetic.

EP359472-A.

21-MAR-1990.

07-SEP-1989: 89EP-0309069.

09-SEP-1988: 88US-0242482.

(LUBR) LUBRIZOL GENETICS.

Adang MJ, Rocheleau TA, Merlo DJ, Murray EE;

WPI: 1990-085243/12.

N-PSDB: AA003587.

Synthetic insecticidal crystal protein gene - comprises DNA sequence encoding insecticidal protein functionally equiv. to bacillus thuringiensis (Bt) insecticidal protein.

Disclosure; ; p: English.

The sequence is that of an insecticidal protein functionally equivalent to a native Bt protein. Plant cells expressing the protein have protection against insect damage. Differences between this sequence and that of the wild type comprise the replacement of Thr(2) and Stop(596) with Ala and Leu resp. and the addn. of 13 AAs to the C-terminus.

Sequence 610 AA:

Query Match 92.4%; Score 595; DB 11; Length 610;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSTTKDVIOKGISVVGDLIGVYGFPGALVSFTYNTFNTIMPSEDPKAF 109

DB 3 ADNNTALDSSTTKDVIOKGISVVGDLIGVYGFPGALVSFTYNTFNTIMPSEDPKAF 62

QY 110 MEQVEALMDOKIADYAKNKALAEIQIQNNVEDYVLSALSMOKNPVSSRNPHSOGRIREL 169

DB 63 MEQVEALMDOKIADYAKNKALAEIQIQNNVEDYVLSALSMOKNPVSSRNPHSOGRIREL 122

QY 170 FSOQESHFRNSMPSFAISGVEVLFLLTYAAANTHLLFLDAQIQYEGEMKYEKEDIAEFY 229

DB 123 FSOQESHFRNSMPSFAISGVEVLFLLTYAAANTHLLFLDAQIQYEGEMKYEKEDIAEFY 182

QY 230 KROKLTQOETDHCVKWYNGLDLKRGSSYESWVNFNRVREMTLYLDLIALFPLDYVR 289

DB 183 KROKLTQOETDHCVKWYNGLDLKRGSSYESWVNFNRVREMTLYLDLIALFPLDYVR 242

QY 290 LYREVEVTELTDRVLDPIYGVNNLRGYGTFSNIENYIKRPHLFDYLRHQFHTPRQPG 349

DB 243 LYREVEVTELTDRVLDPIYGVNNLRGYGTFSNIENYIKRPHLFDYLRHQFHTPRQPG 302

QY 350 YYGNDSEFNYSNGVYSTRPSIGSMDITSPYGNKSSSEPONLEFNEKRYRAVANNTLA 409

DB 303 YYGNDSEFNYSNGVYSTRPSIGSMDITSPYGNKSSSEPONLEFNEKRYRAVANNTLA 362

QY 410 VMSAVYSGVTKVEFSGYNDQTEASTQYDSCRNNGAVSWSDIDLPETTDEPLEKGY 469

DB 363 VMSAVYSGVTKVEFSGYNDQTEASTQYDSCRNNGAVSWSDIDLPETTDEPLEKGY 422

QY 470 SHOLNVMCFLMOGSNGRTIPVLTWTHKSVDFEWMIDSKRTLOPLKAVKILGSGASVAG 529

DB 423 SHOLNVMCFLMOGSNGRTIPVLTWTHKSVDFEWMIDSKRTLOPLKAVKILGSGASVAG 482

QY 530 PRFTGGDIIOCTENGSAATLYVTPDVYSQKRYRARIHYASTSQIFPTLSIDGAPFNQYF 589

DB 483 PRFTGGDIIOCTENGSAATLYVTPDVYSQKRYRARIHYASTSQIFPTLSIDGAPFNQYF 542

QY 590 DKTIKNGDTLTYNSFNLASFSTPELISGNLQIGVTGLSAGDKVYIDKIEFIPVN 644

DB 543 DKTIKNGDTLTYNSFNLASFSTPELISGNLQIGVTGLSAGDKVYIDKIEFIPVN 597

RESULT 12

AAW00333

ID AAW00333 standard; protein: 610 AA.

AAW00333:

02-JAN-1997 (first entry)

Bacillus thuringiensis pesticidal protein toxin (synthetic).

Bacillus thuringiensis; plant; codon; crystal protein; Btl gene;

KW toxin; insect; pest; tobacco hornworm.

OS Bacillus thuringiensis.

PN US5567600-A.

PD 22-OCT-1996.

PF 24-SEP-1983: 83US-0535354.

PR 06-JAN-1995: 95US-0369835.

PR 24-SEP-1983: 83US-0535354.

PR 04-APR-1986: 86US-0848733.

PR 09-SEP-1988: 88US-0242482.

PR 28-JAN-1992: 92US-0827844.

PR 03-MAY-1993: 93US-0057191.

PA (MYCO) MYCOGEN PLANT SCI INC.

PI Adang MJ, Merlo DJ, Murray EE, Rocheleau TA;

PI WPI: 1996-484994/48.

DR N-PSDB: AAT40340.

XX

Increasing Bacillus thuringiensis gene expression in plants - by reducing frequency of codon usages that are rare in plants

Disclosure; Fig 1: 23pp; English.

The synthetic Btl gene sequence (AAT40340) differs from the native sequence as found in p544Pst-Met5 (AAT40341). Changes in amino acids occur in the synthetic sequence with alanine replacing threonine at CC residue 2 and leucine replacing the stop at residue 596 followed by CC the addition of 13 amino acids at the C-terminus.

At least 32% of the codons and/or at least 11% of the nucleotides in the coding sequence of the native Btl gene are changed.

By avoiding codon usage that are rare in plants, plants that have more Btl crystal protein than plants contrg. the native Btl gene, and are thus more toxic to insect pests such as tobacco hornworm, can be produced.

Sequence 610 AA:

Query Match 92.4%; Score 595; DB 17; Length 610;

Best Local Similarity 100.0%: Pred. No. 0:
Matches 595: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 50 ADNNTALDSSSTTKDVIQKGISVGGDLGCVGFPFGALVSFTYNFLNTIMPSEDPKAKF 109
    |||||||
DB 3 ADNNTALDSSSTTKDVIQKGISVGGDLGCVGFPFGALVSFTYNFLNTIMPSEDPKAKF 62
    |||||||
OY 110 MEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 169
    |||||||
DB 63 MEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 122
    |||||||
OY 170 FSOAESHFNRNMPSPFALSISGEVLEFTTYAQANTHLFLKDAQIYGEEMGEKEEDIAEFY 229
    |||||||
DB 123 FSOAESHFNRNMPSPFALSISGEVLEFTTYAQANTHLFLKDAQIYGEEMGEKEEDIAEFY 182
    |||||||
OY 230 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVR 289
    |||||||
DB 183 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVR 242
    |||||||
OY 290 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNTIENTYRKPHLFDYLHRIQFTRPOG 349
    |||||||
DB 243 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNTIENTYRKPHLFDYLHRIQFTRPOG 302
    |||||||
OY 350 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLA 409
    |||||||
DB 303 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLA 362
    |||||||
OY 410 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 469
    |||||||
DB 363 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 422
    |||||||
OY 470 SHOLNVMCFILOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVYKAKKLOGSASVYAG 529
    |||||||
DB 423 SHOLNVMCFILOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVYKAKKLOGSASVYAG 482
    |||||||
OY 530 PRFTGGDIIOCTENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYIF 589
    |||||||
DB 483 PRFTGGDIIOCTENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYIF 542
    |||||||
OY 590 DKTINKGDTLTYSFNFLASFSTPELSSGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
    |||||||
DB 543 DKTINKGDTLTYSFNFLASFSTPELSSGNLQIGVTGLSAGDKVYIDKIEFIPVN 597
    |||||||

```

RESULT 13

AA69667 standard; Protein: 610 AA.

```

ID AA69667
AC AA69667
XX
XX
DT 08-MAY-2000 (first entry)
XX
DE Bacillus thuringiensis (Bt) toxin encoded by synthetic Bt gene.
XX
KW Bt toxin; codon usage; expression; transgenic plant; pesticide;
XX
KW Insecticide; mutant; mutcin.
XX
OS Bacillus thuringiensis var. tenebrionis.
XX
OS Synthetic.
XX
PN US6015891-A.
XX
PD 18-JAN-2000.
XX
PF 29-AUG-1996; 96US-0705438.
XX
PR 06-JAN-1995; 95US-0369835.
PR 09-SEP-1988; 88US-0242482.
PR 28-JAN-1992; 92US-0827844.
PR 03-MAY-1993; 93US-0057191.
XX
XX (MYCO ) MYCOGEN PLANT SCI INC.
XX

```

PI Murray EE, Adang MJ;
XX WPI, 2000-136460/12.
DR N-PSDB; AA69667.
XX
PT Synthetic Bacillus thuringiensis pesticidal toxin gene for expression
in plant cells has coding sequence adapted to codon usage bias of
plants -
XX
XX Example 3; Fig 1A-C; 29pp; English.
PS
SS
CC This sequence represents a Bacillus thuringiensis (Bt) toxin encoded by
a synthetic Bt gene (AA59994). This gene is expressed at a high level
in descendant plant cells and encodes a pesticidal protein toxin. The
synthetic gene was designed to be expressed in plants at a higher level
than wild-type Bt genes (e.g., AA59993). This was accomplished by
altering the DNA sequence of the native Bt gene such that it contained
codons preferred by highly expressed plant genes, had an A+T content
comparable to that found in plant genes and contained a plant initiation
sequence. Additionally, sequences that cause destabilization,
inappropriate polyadenylation, degradation and termination of RNA were
eliminated, and sequences that constitute RNA hairpin and splice sites
were avoided. The resulting synthetic Bt gene has at least 10% of its
nucleotides altered as compared with the native Bt gene. The synthetic Bt
gene is operably linked to a plant-expressible promoter and can be
transformed into plant cells. The gene is used to produce transgenic
plants having resistance to pests, particularly insects. The
modifications produced in the coding sequence increases the level of
expression of Bt toxin in plants.

Sequence 610 AA:

Query Match 92.4%: Score 595; DB 21; Length 610;

Best Local Similarity 100.0%: Pred. No. 0:
Matches 595: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 50 ADNNTALDSSSTTKDVIQKGISVGGDLGCVGFPFGALVSFTYNFLNTIMPSEDPKAKF 109
    |||||||
DB 3 ADNNTALDSSSTTKDVIQKGISVGGDLGCVGFPFGALVSFTYNFLNTIMPSEDPKAKF 62
    |||||||
OY 110 MEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 169
    |||||||
DB 63 MEQVEALMDOKIADYAKKALAELOGLONNVEDYVSALSMQKNPVSSRNPHSGRIREL 122
    |||||||
OY 170 FSOAESHFNRNMPSPFALSISGEVLEFTTYAQANTHLFLKDAQIYGEEMGEKEEDIAEFY 229
    |||||||
DB 123 FSOAESHFNRNMPSPFALSISGEVLEFTTYAQANTHLFLKDAQIYGEEMGEKEEDIAEFY 182
    |||||||
OY 230 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVR 289
    |||||||
DB 183 KROLKLTQETDHCVKWYNVGLDKLRGSSYESWVNFNRRREMTLVLDLALFPLYDVR 242
    |||||||
OY 290 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNTIENTYRKPHLFDYLHRIQFTRPOG 349
    |||||||
DB 243 LYPKEVKTELTRDVLTDPIVGNVNLRGYGTTSNTIENTYRKPHLFDYLHRIQFTRPOG 302
    |||||||
OY 350 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLA 409
    |||||||
DB 303 YYGNDSEFNWWSGNVYSTRPSIGSNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLA 362
    |||||||
OY 410 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 469
    |||||||
DB 363 WPSAVYSGVTKVFEFSQYNDQTDASTQTYDSKRNAGVSWDSIDQLPETTDEPLEKGY 422
    |||||||
OY 470 SHOLNVMCFILOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVYKAKKLOGSASVYAG 529
    |||||||
DB 423 SHOLNVMCFILOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVYKAKKLOGSASVYAG 482
    |||||||
OY 530 PRFTGGDIIOCTENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYIF 589
    |||||||
DB 483 PRFTGGDIIOCTENGSAATITVTPDVYSQKYRARIHYASTQITFTLSLDGAPFNQYIF 542
    |||||||
OY 590 DKTINKGDTLTYSFNFLASFSTPELSSGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
    |||||||

```

```

Db 543 DKTINKGDTLYNSFNFLASFSTPELSCNNLQIGVTGLSAGDKYIDKIEFTIPVN 597
|||||
RESULT 14
AAR15784 standard; Protein: 956 AA.
XX AAR15784
AC AAR15784;
XX 10-FEB-1992 (first entry)
DE B.thuringiensis toxin/AcNPV gp64 fusion protein.
XX chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae;
XX midgut targeting; bacterial endotoxin; pfx7.
XX Bacillus thuringiensis var. tenebriosis.
XX Autographa californica Nuclear Polyhedrosis Virus.
XX MO9117254-A.
XX 14-NOV-1991.
XX 02-MAY-1991; 91MO-US03008.
XX 03-MAY-1990; 90US-0518575.
XX (REGC ) UNIV OF CALIFORNIA.
XX Sivasubramanian N, Federici A;
XX WPI: 1991-353775/48.
XX N-PSDB: AAQ14806.
XX Extending host range or toxicity of insecticidal proteins - using
XX protein capable of binding to gut epithelium of insects
XX Claim 55; Fig 17; 61pp; English.
XX A polylinker was inserted into the XmnI restriction site at the
XX carboxyl terminus coding region of B.thuringiensis var. tenebriosis
XX (Bt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV
XX was operably linked to the Bt toxin coding sequence via the
XX polylinker. The gp64 gene sequences act as midgut targeting
XX signals for bacterial endotoxins. Plasmid pFX7 was one of three
XX different Bt/gp64 gene fusions that were constructed and its
XX deduced amino acid sequence is given here.
XX See also AAQ14806 and AAQ14808.
XX
XX Sequence 956 AA:
Query Match 91.6%; Score 590; DB 12; Length 956;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 50 AANNTEALDSSSTTKVIOKIGISVGDGLGVGFPFGALVSYTYTNFLMTIPSEDPKMAF 109
DB 16 AANNTEALDSSSTTKVIOKIGISVGDGLGVGFPFGALVSYTYTNFLMTIPSEDPKMAF 75
OY 110 MEQVEALMDOKIADYAKKNAELGLONNVEDYVSALSSMOKNPVSSRNPHSOGRIEEL 169
DB 76 MEQVEALMDOKIADYAKKNAELGLONNVEDYVSALSSMOKNPVSSRNPHSOGRIEEL 135
OY 170 FSOAESHFNSMPSFAISGEVLTFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFY 229
DB 136 FSOAESHFNSMPSFAISGEVLTFTTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFY 195
OY 230 KROLKLTQYTYDHCYKMYWVGDKLKGSSYSEWVFNRRRMTLTIVDLALFPLYOVR 289
DB 196 KROLKLTQYTYDHCYKMYWVGDKLKGSSYSEWVFNRRRMTLTIVDLALFPLYOVR 255
OY 290 LVPKEVTELTBDVLTDPVGVNMLRGYGTFSNIENYIRKPHLPDYLRHQFHTRFQPG 349

```

```

Db 256 LVPKEVTELTBDVLTDPVGVNMLRGYGTFSNIENYIRKPHLPDYLRHQFHTRFQPG 315
|||||
RESULT 15
AAR15783 standard; Protein: 1100 AA.
XX AAR15783;
XX 10-FEB-1992 (first entry)
DE B.thuringiensis toxin/AcNPV gp64 fusion protein.
XX chimeric; fusion protein; insecticide; AcNPV; Lepidoptera larvae;
XX midgut targeting; bacterial endotoxin; pFAV10.
XX Bacillus thuringiensis var. tenebriosis.
XX Autographa californica Nuclear Polyhedrosis Virus.
XX MO9117254-A.
XX 14-NOV-1991.
XX 02-MAY-1991; 91MO-US03008.
XX 03-MAY-1990; 90US-0518575.
XX (REGC ) UNIV OF CALIFORNIA.
XX Sivasubramanian N, Federici A;
XX WPI: 1991-353775/48.
XX N-PSDB: AAQ14806.
XX Extending host range or toxicity of insecticidal proteins - using
XX protein capable of binding to gut epithelium of insects
XX Claim 55; Fig 16; 61pp; English.
XX A polylinker was inserted into the XmnI restriction site at the
XX carboxyl terminus coding region of B.thuringiensis var. tenebriosis
XX (Bt) toxin. DNA encoding the gp64 viral membrane protein of AcNPV
XX was operably linked to the Bt toxin coding sequence via the
XX polylinker. The gp64 gene sequences act as midgut targeting
XX signals for bacterial endotoxins. Of three different Bt/gp64 gene
XX fusions that were constructed, pFAV10 was the longest. Its deduced
XX amino acid sequence is given here.
XX See also AAQ14807 and AAQ14808.
XX
XX Sequence 1100 AA:
Query Match 91.6%; Score 590; DB 12; Length 1100;

```

Best Local Similarity 100.0%; Pred. No. 0;
Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 50 ADNNTEALDSSTTKDYIQGIVSGVGLLCVGFPGGALVSYTYNFLTNTIMPSDEPKAF 109
    |||
Db 16 ADNNTEALDSSTTKDYIQGIVSGVGLLCVGFPGGALVSYTYNFLTNTIMPSDEPKAF 75
QY 110 MEQVEALMDOKIADYAKKNAELQGLQNNVEDYVSAISSMOKNPVSSNPHSOGRIPL 169
    |||
Db 76 MEQVEALMDOKIADYAKKNAELQGLQNNVEDYVSAISSMOKNPVSSNPHSOGRIPL 135
QY 170 FSGAESHFNRNMPFSAISGEVLFLLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEY 229
    |||
Db 136 FSGAESHFNRNMPFSAISGEVLFLLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEY 195
QY 230 KRQKLTQETDHCWKVYVNGDLKLGSSYESKVNENRYRREMTLTVLDLALFPLYDVR 289
    |||
Db 196 KRQKLTQETDHCWKVYVNGDLKLGSSYESKVNENRYRREMTLTVLDLALFPLYDVR 255
QY 290 LYPKEVKTETLRDYLTPIVGVNNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQPG 349
    |||
Db 256 LYPKEVKTETLRDYLTPIVGVNNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQPG 315
QY 350 YYGNDSPFNWMSGNYVSTRSISNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLA 409
    |||
Db 316 YYGNDSPFNWMSGNYVSTRSISNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLA 375
QY 410 WPSAYSVGVKVEFSQYNDQDEASTQYTDKRNAGVSWDSIDOLPETTDEPLEKGY 469
    |||
Db 376 WPSAYSVGVKVEFSQYNDQDEASTQYTDKRNAGVSWDSIDOLPETTDEPLEKGY 435
QY 470 SHQNLVWVGLMGSRGITPVLWTHKSVDFNMIDSKITLOPLVKAVKLGSGAVYAG 529
    |||
Db 436 SHQNLVWVGLMGSRGITPVLWTHKSVDFNMIDSKITLOPLVKAVKLGSGAVYAG 495
QY 530 PRFTGDDIIOCTBENGSAATITVTPDVYSQKTRARIHVASTSQITFTLSLDGAPNQYFF 589
    |||
Db 496 PRFTGDDIIOCTBENGSAATITVTPDVYSQKTRARIHVASTSQITFTLSLDGAPNQYFF 555
QY 590 DKTINKGDTLTYNSEFLASFSTPFELSGNNLQIGVTLGASGAKYVIDXIE 639
    |||
Db 556 DKTINKGDTLTYNSEFLASFSTPFELSGNNLQIGVTLGASGAKYVIDXIE 605

RESULT 16
AAR99960
ID AAR99960 standard: Protein: 644 AA.
AC AAR99960:
DT 04-DEC-1996 (first entry)
XX
XX B.t.t. coleopteran toxin (alternative N- and C-terminal truncations).
DE
XX Bacillus thuringiensis var. tenebrionis; insect resistance;
KM transgenic plant; crop protection; crystal protein; toxin;
KW Coleoptera.
XX
XX Bacillus thuringiensis var. tenebrionis.
OS
XX
XX Key Location/Qualifiers
FH MISC-difference 48 /note= "N-terminus of construct 5456"
FT MISC-difference 77 /note= "N-terminus of construct 5452"
FT MISC-difference 99 /note= "N-terminus of construct 5467"
FT MISC-difference 490 /note= "C-terminus of construct 5438"
FT MISC-difference 536 /note= "C-terminus of construct 5441"
FT MISC-difference 582 /note= "C-terminus of construct 5449"
FT

```

```

FT MISC-difference 640 /note= "C-terminus of construct 5448"
ET
XX
XX EP731170-A1.
XX
XX 11-SEP-1996.
XX
XX 26-APR-1988; 88EP-0870070.
XX
XX 29-APR-1987; 87US-0044081.
XX
XX (MONS ) MONSANTO CO.
XX
XX Fischhoff DA, Fuchs RL, Lavrik PB, McPherson SA;
XX Perlak FJ;
XX WPI: 1996-403991/41.
XX
XX Chimeric plant gene which expresses a Bacillus thuringiensis toxin
XX protein - useful for prodn. of plants which are toxic to
XX Coleopteran insects
XX
XX Disclosure: Fig 10; 72pp; English.
XX
XX The effects of N- and C-terminal deletions (AAR99960) on the toxicity
XX of the Coleopteran toxin (see also AAR99958) of Bacillus thuringiensis
XX var. tenebrionis (B.t.t.) were examined. Mutant genes were expressed
XX in E. coli and the truncated proteins were tested for activity against
XX Colorado potato beetle. All the C-terminal truncations, even of
XX only 4 amino acids (construct 5448), resulted in a loss of activity.
XX The N-terminus of the toxin was more tolerant; a mutant toxin
XX deleted of 76 amino acids (construct 5452) exhibited toxicity.
XX However, a deletion of 99 amino acids (construct 5467) resulted in
XX loss of activity.
XX
XX Sequence 644 AA:
XX
XX Query Match 84.3%; Score 543; DB 17; Length 644;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDTIKTTENNEVPTNHVQPLAETPPTLEDLNYKEFLMTADNNTALDSS 60
    |||
Db 1 MNPNNRSEHDTIKTTENNEVPTNHVQPLAETPPTLEDLNYKEFLMTADNNTALDSS 60
QY 61 TTKVYIQGISVVGDLGCVGFPGGALVSYTYNFLTNTIMPSDEPKAFMEQVEALMDOK 120
    |||
Db 61 TTKVYIQGISVVGDLGCVGFPGGALVSYTYNFLTNTIMPSDEPKAFMEQVEALMDOK 120
QY 121 IADYAKKNAELQGLQNNVEDYVSAISSMOKNPVSSRNPHSOGRIRELFSGAESHFNRN 180
    |||
Db 121 IADYAKKNAELQGLQNNVEDYVSAISSMOKNPVSSRNPHSOGRIRELFSGAESHFNRN 180
QY 181 MPFSAISGEVLFLLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEYKRQKLTQEXT 240
    |||
Db 181 MPFSAISGEVLFLLTYAQAANTHLFLKDAQIYGEEMGEKEDIAEYKRQKLTQEXT 240
QY 241 DHCYKWNVGLDKRGSSYESVWVFNRYRREMTLTVLDLALFPLYDVRLYPREVTELT 300
    |||
Db 241 DHCYKWNVGLDKRGSSYESVWVFNRYRREMTLTVLDLALFPLYDVRLYPREVTELT 300
QY 301 RDVLTDPVGVNNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQPGYYGNDSPFNYS 360
    |||
Db 301 RDVLTDPVGVNNLRGYGTFSNIENTYIRKPHLFDYLHRIQFHTRFQPGYYGNDSPFNYS 360
QY 361 GNYVSTRSISGNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLAWPSAVYSGVT 420
    |||
Db 361 GNYVSTRSISGNDIITSPFYGNKSSPEVQNLFEENGKAVYRAVANTNLAWPSAVYSGVT 420
QY 421 KVERSQYNDQDEASTQYTDKRNAGVSWDSIDOLPETTDEPLEKGSYSHQNLVWVCL 480
    |||
Db 421 KVERSQYNDQDEASTQYTDKRNAGVSWDSIDOLPETTDEPLEKGSYSHQNLVWVCL 480

```

CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

Query 1 MNPNNSEHDTITTTENNEVPTNHVOYPLAETPTPLDNLNKEFLRMADNNTALDSS 60
 Db 1 MNPNNSEHDTITKTENNEVPTNHVOYPLAETPTPLDNLNKEFLRMADNNTALDSS 60
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 61 TTKDVLOKGSIVYGDLLGVGPPFGALVSFYTNFLTTPSPDPPKAKMEQVEALMDOK 120
 Db 61 TTKDVLOKGSIVYGDLLGVGPPFGALVSFYTNFLTTPSPDPPKAKMEQVEALMDOK 120
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 121 IADYAKKALAELOGLQNNVEDYVSLSSWQKNPVSSRNPHSGRIREFSQASHFRNS 180
 Db 121 IADYAKKALAELOGLQNNVEDYVSLSSWQKNPVSSRNPHSGRIREFSQASHFRNS 180
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 181 MPSPALSGEYVLELTYYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROKLQOXYT 240
 Db 181 MPSPALSGEYVLELTYYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROKLQOXYT 240
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 241 DHCKKYNVAGIDKRGSSYSESWNENRYREMTLTVDLALPLVDVRLYPREVKTELT 300
 Db 241 DHCKKYNVAGIDKRGSSYSESWNENRYREMTLTVDLALPLVDVRLYPREVKTELT 300
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 301 RDVLTDPVGNVNLRGYGTFSNIENYIRKPHLEDYLHRIQFHTRPQGYGNDSEFNYS 360
 Db 301 RDVLTDPVGNVNLRGYGTFSNIENYIRKPHLEDYLHRIQFHTRPQGYGNDSEFNYS 360
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 361 GNYVSTRPSIGSNDITISPEYGNKSSPEVONLEFNKGYRAYANTNLAWPSAVYSGVT 420
 Db 361 GNYVSTRPSIGSNDITISPEYGNKSSPEVONLEFNKGYRAYANTNLAWPSAVYSGVT 420
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 421 KVEFSQYNDQDEASTQYDTSKRNVGAVSWSIDQLPPTTDEPLEKGYSHQNLVWCFL 480
 Db 421 KVEFSQYNDQDEASTQYDTSKRNVGAVSWSIDQLPPTTDEPLEKGYSHQNLVWCFL 480
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 481 MQSGRGITPVLWTWHKSVDFENMIDSKKITQLPLVKAYKLQSGASVYVAGPRTGGDIIOG 540
 Db 481 MQSGRGITPVLWTWHKSVDFENMIDSKKITQLPLVKAYKLQSGASVYVAGPRTGGDIIOG 540
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 541 TENGSAATIIYTPDVYSQKRYRARIHYASTQSITFTSLDGAPPNQYFPDKTINKGDTLT 600
 Db 541 TENGSAATIIYTPDVYSQKRYRARIHYASTQSITFTSLDGAPPNQYFPDKTINKGDTLT 600
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 601 YNSFNILASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Db 601 YNSFNILASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 18
 ID AAW34812 standard; Protein: 644 AA.
 AC AAW34812:
 DE 25-FEB-1998 (first entry)
 KW Novel CryIIIA mutant protein L251A.
 KM CryIIIA gene: corn rootworm toxicity; CryIIIA protein:
 increased toxicity; Coleopteran insect; Colorado potato beetle;
 relative solvent accessibility; plant resistance;
 Diabrotica virgifera virgifera.
 OS Synthetic.
 PS Bacillus thuringiensis.
 CC

CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

Query 1 MNPNNSEHDTITTTENNEVPTNHVOYPLAETPTPLDNLNKEFLRMADNNTALDSS 60
 Db 1 MNPNNSEHDTITKTENNEVPTNHVOYPLAETPTPLDNLNKEFLRMADNNTALDSS 60
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 61 TTKDVLOKGSIVYGDLLGVGPPFGALVSFYTNFLTTPSPDPPKAKMEQVEALMDOK 120
 Db 61 TTKDVLOKGSIVYGDLLGVGPPFGALVSFYTNFLTTPSPDPPKAKMEQVEALMDOK 120
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 121 IADYAKKALAELOGLQNNVEDYVSLSSWQKNPVSSRNPHSGRIREFSQASHFRNS 180
 Db 121 IADYAKKALAELOGLQNNVEDYVSLSSWQKNPVSSRNPHSGRIREFSQASHFRNS 180
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 181 MPSPALSGEYVLELTYYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROKLQOXYT 240
 Db 181 MPSPALSGEYVLELTYYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROKLQOXYT 240
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 241 DHCKKYNVAGIDKRGSSYSESWNENRYREMTLTVDLALPLVDVRLYPREVKTELT 300
 Db 241 DHCKKYNVAGIDKRGSSYSESWNENRYREMTLTVDLALPLVDVRLYPREVKTELT 300
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 301 RDVLTDPVGNVNLRGYGTFSNIENYIRKPHLEDYLHRIQFHTRPQGYGNDSEFNYS 360
 Db 301 RDVLTDPVGNVNLRGYGTFSNIENYIRKPHLEDYLHRIQFHTRPQGYGNDSEFNYS 360
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 361 GNYVSTRPSIGSNDITISPEYGNKSSPEVONLEFNKGYRAYANTNLAWPSAVYSGVT 420
 Db 361 GNYVSTRPSIGSNDITISPEYGNKSSPEVONLEFNKGYRAYANTNLAWPSAVYSGVT 420
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 421 KVEFSQYNDQDEASTQYDTSKRNVGAVSWSIDQLPPTTDEPLEKGYSHQNLVWCFL 480
 Db 421 KVEFSQYNDQDEASTQYDTSKRNVGAVSWSIDQLPPTTDEPLEKGYSHQNLVWCFL 480
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 481 MQSGRGITPVLWTWHKSVDFENMIDSKKITQLPLVKAYKLQSGASVYVAGPRTGGDIIOG 540
 Db 481 MQSGRGITPVLWTWHKSVDFENMIDSKKITQLPLVKAYKLQSGASVYVAGPRTGGDIIOG 540
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 541 TENGSAATIIYTPDVYSQKRYRARIHYASTQSITFTSLDGAPPNQYFPDKTINKGDTLT 600
 Db 541 TENGSAATIIYTPDVYSQKRYRARIHYASTQSITFTSLDGAPPNQYFPDKTINKGDTLT 600
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 601 YNSFNILASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Db 601 YNSFNILASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 18
 ID AAW34812 standard; Protein: 644 AA.
 AC AAW34812:
 DE 25-FEB-1998 (first entry)
 KW Novel CryIIIA mutant protein L251A.
 KM CryIIIA gene: corn rootworm toxicity; CryIIIA protein:
 increased toxicity; Coleopteran insect; Colorado potato beetle;
 relative solvent accessibility; plant resistance;
 Diabrotica virgifera virgifera.
 OS Synthetic.
 PS Bacillus thuringiensis.
 CC

```

FH Key Location/Qualifiers
FT MISC-difference 251 /label= L251A
FT /note= "wild type Leu replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34813-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX and can be used to combat, or improve plant resistance towards Diabrotica
XX virgifera virgifera the toxicity of the present sequence towards Diabrotica
XX 50% feeding inhibition is observed). The EC50 value (concentration at which
XX be 5.27 microgram per millilitre, compared to 7.45 microgram per
XX millilitre for the wild type CryIIIA protein.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 644 AA:
SQ
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPNNRSHDITKTENNVEPTNHVOYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
DB 1 MNPNNRSHDITKTENNVEPTNHVOYPLAETPNPTLEDLNYKEFLRMADNNTALDSS 60
QY 61 TTKDVIOKGISVVDLGVGFPFGALVSYFTNLTNTPSDEPKAFMEQVVALMDOK 120
DB 61 TTKDVIOKGISVVDLGVGFPFGALVSYFTNLTNTPSDEPKAFMEQVVALMDOK 120
QY 121 IADYAKKNAELQGLONNVEDYVSAISMQKNPSSRNPHSOGRIEELFSQAESHPRNS 180
DB 121 IADYAKKNAELQGLONNVEDYVSAISMQKNPSSRNPHSOGRIEELFSQAESHPRNS 180
QY 121 IADYAKKNAELQGLONNVEDYVSAISMQKNPSSRNPHSOGRIEELFSQAESHPRNS 180
DB 121 IADYAKKNAELQGLONNVEDYVSAISMQKNPSSRNPHSOGRIEELFSQAESHPRNS 180
QY 181 MPFAISGIEVLELTYYAOAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEXT 240
DB 181 MPFAISGIEVLELTYYAOAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEXT 240
QY 181 MPFAISGIEVLELTYYAOAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEXT 240
DB 181 MPFAISGIEVLELTYYAOAANTHLFLKDAQIYGEEMGYEKEDIAEFYRQLKLTQEXT 240
QY 241 DHCKWYNVGLDKRGSSYSWVNFNRYRREMTLTVDLALPLVYRKYRPREVKTELT 300
DB 241 DHCKWYNVGLDKRGSSYSWVNFNRYRREMTLTVDLALPLVYRKYRPREVKTELT 300
QY 301 RDVLTDPYGVNMLRGYGTFSNIENTYRKPHELDYLRHQFTRPOPGYGGNDSFNYS 360
DB 301 RDVLTDPYGVNMLRGYGTFSNIENTYRKPHELDYLRHQFTRPOPGYGGNDSFNYS 360

```

```

QY 361 GNYVSTRPSIGSNDITTSPEYGNKSSPEVONLEPNEGKAVYRAVANINLAWPSAVISGVT 420
DB 361 GNYVSTRPSIGSNDITTSPEYGNKSSPEVONLEPNEGKAVYRAVANINLAWPSAVISGVT 420
QY 421 KVEFSQYNDQDEASTQTYDSKRNAGVASMDSIDQLPETTDEPLEKGYSHOLNYYWCFL 480
DB 421 KVEFSQYNDQDEASTQTYDSKRNAGVASMDSIDQLPETTDEPLEKGYSHOLNYYWCFL 480
QY 481 MOGSRGTIPVLTWTHKSVDFFNMIDSKRTQLPLVKAAYKLOSASVAVGPRFTGDIIOG 540
DB 481 MOGSRGTIPVLTWTHKSVDFFNMIDSKRTQLPLVKAAYKLOSASVAVGPRFTGDIIOG 540
QY 541 TENSSAATYVTPDVYSOKYRARIHASTSQITFTLSLDCGAPPNQYFPKTKNKDITLT 600
DB 541 TENSSAATYVTPDVYSOKYRARIHASTSQITFTLSLDCGAPPNQYFPKTKNKDITLT 600
QY 601 YNSFNLSFSTPELSCNNLQIGVTGLSADKVIYDIKEIFIPVN 644
DB 601 YNSFNLSFSTPELSCNNLQIGVTGLSADKVIYDIKEIFIPVN 644
RESULT 19
AAW34813
ID AAW34813 standard; Protein; 644 AA.
AC AAW34813:
DT 25-FEB-1998 (first entry)
XX
XX Novel CryIIIA mutant protein G352A.
XX
XX CryIIIA gene: corn rootworm toxicity; CryIIIA protein:
XX increased toxicity; Coleopteran insect; Colorado potato beetle;
XX Diabrotica virgifera virgifera.
XX
XX Synthetic.
XX Bacillus thuringiensis.
OS
OS
FH Key Location/Qualifiers
FT MISC-difference 352 /label= G352A
FT /note= "wild type Gly replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34813-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

```


CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards *Diabrotica*
 CC *virgifera* was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 4.11 microgram per millilitre, compared to 7.45 microgram per
 CC millilitre for the wild type *CryIIIA* protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTKTENNENPTNHVOYPLAETPNPTLEDLNKKEFLRMADNNTTEALDSS 60
 DB 1 MNPNNSEHDTKTENNENPTNHVOYPLAETPNPTLEDLNKKEFLRMADNNTTEALDSS 60
 QY 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTWPSDEPKAKMEQVEALMDOK 120
 DB 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTWPSDEPKAKMEQVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNEDVYVALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
 DB 121 IADYAKKALAELOGLONNEDVYVALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
 QY 181 MPFSAISGYEVLEFLTYAQAANTHFLFLKDAQYGEWGEKEDIKFKRQKLQOXYT 240
 DB 181 MPFSAISGYEVLEFLTYAQAANTHFLFLKDAQYGEWGEKEDIKFKRQKLQOXYT 240
 QY 241 DHCWKYTNVGLDKLRGSSYSWVNFNRYRREMTLVLDIALFPLVDVRLYPREVTELT 300
 DB 241 DHCWKYTNVGLDKLRGSSYSWVNFNRYRREMTLVLDIALFPLVDVRLYPREVTELT 300
 QY 301 RDVLTIDYGVNNLRGCTFSNENYIRKPHLEFDYLRHQFHTRFQPGYGGNDSFYMS 360
 DB 301 RDVLTIDYGVNNLRGCTFSNENYIRKPHLEFDYLRHQFHTRFQPGYGGNDSFYMS 360
 QY 361 GNYVSTRPSIGSNDITSPYGNKSEPPVONLEFNGEKYRVAANTNLAWPSAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITSPYGNKSEPPVONLEFNGEKYRVAANTNLAWPSAVYSGVT 420
 QY 421 KVESQYNDQDEASTQYTSKRNVGAVSMDSIDQLPETTDEPLEGYSHOLNYYWVCF 480
 DB 421 KVESQYNDQDEASTQYTSKRNVGAVSMDSIDQLPETTDEPLEGYSHOLNYYWVCF 480
 QY 481 MGSRGITPVLTWTHKSVDFEENMIDSKKITQLPLVKAYKLQSGASVAVAGPRTGGDIIQC 540
 DB 481 MGSRGITPVLTWTHKSVDFEENMIDSKKITQLPLVKAYKLQSGASVAVAGPRTGGDIIQC 540
 QY 541 TENGSAATYTPDVYSQYKRAIRIHASTSQTFTLSDGAPRNOYFPKTIKGGTTL 600
 DB 541 TENGSAATYTPDVYSQYKRAIRIHASTSQTFTLSDGAPRNOYFPKTIKGGTTL 600
 QY 601 YNSFNLASFTPELSGNNLOIGYGLSAGDKYIIDKIEFIPVN 644
 DB 601 YNSFNLASFTPELSGNNLOIGYGLSAGDKYIIDKIEFIPVN 644

RESULT 20

AAW34814 ID AAW34814 standard; Protein: 644 AA.

AAW34814:

25-FEB-1998 (first entry)

Novel *CryIIIA* mutant protein N353A.

KM *CryIIIA* gene: corn rootworm toxicity; *CryIIIA* protein:
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;

KM *Diabrotica virgifera virgifera*.

XX Synthetic.
 OS *Bacillus thuringiensis*.

XX Key Location/Qualifiers

FT Misc-difference 353 /label= N353A
 FT /note= "wild type Asn replaced with Ala"

PN US5659123-A.

PD 19-AUG-1997.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

PA (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Jansens S, Peferoen M, Van Rie J;

DR WPI: 1997-424316/39.

PT Modified *Bacillus thuringiensis* *CryIIIA* proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

XX Example 1; Page -: 22pp; English.

CC Novel *CryIIIA* proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the *CryIIIA* protein of *Bacillus*
 CC *thuringiensis*. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel *CryIIIA* proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards *Diabrotica*
 CC *virgifera* was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 5.21 microgram per millilitre, compared to 11.60 microgram per
 CC millilitre for the wild type *CryIIIA* protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTKTENNENPTNHVOYPLAETPNPTLEDLNKKEFLRMADNNTTEALDSS 60
 DB 1 MNPNNSEHDTKTENNENPTNHVOYPLAETPNPTLEDLNKKEFLRMADNNTTEALDSS 60
 QY 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTWPSDEPKAKMEQVEALMDOK 120
 DB 61 TTKDVIOKGISVVGDLGVGFPFGALVSFTYNTFNTWPSDEPKAKMEQVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNEDVYVALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
 DB 121 IADYAKKALAELOGLONNEDVYVALSSWQKNPVSSRNPHSGRIRELFSQAESHFRNS 180
 QY 181 MPFSAISGYEVLEFLTYAQAANTHFLFLKDAQYGEWGEKEDIKFKRQKLQOXYT 240
 DB 181 MPFSAISGYEVLEFLTYAQAANTHFLFLKDAQYGEWGEKEDIKFKRQKLQOXYT 240
 QY 241 DHCWKYTNVGLDKLRGSSYSWVNFNRYRREMTLVLDIALFPLVDVRLYPREVTELT 300
 DB 241 DHCWKYTNVGLDKLRGSSYSWVNFNRYRREMTLVLDIALFPLVDVRLYPREVTELT 300

```

QY 301 RDVLTDPVGNVNNRGYGTFTFSNIENIRKPHLFEDYLRHQFTFRQPGYGGDSFNWMS 360
    |||
Dd 301 RDVLTDPVGNVNNRGYGTFTFSNIENIRKPHLFEDYLRHQFTFRQPGYGGDSFNWMS 360
QY 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
    |||
Dd 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
QY 421 KVEFSQVNDQTDASTQTYDSKRNKAVSWDSIDQLPETTDEPLEKGYSHQNLNVMCF 480
    |||
Dd 421 KVEFSQVNDQTDASTQTYDSKRNKAVSWDSIDQLPETTDEPLEKGYSHQNLNVMCF 480
QY 481 MGSRGITPVLWTHTKSVDFNNMIDSKKITQLPLVAKYKLGASAVVAGPRFTGGDIIC 540
    |||
Dd 481 MGSRGITPVLWTHTKSVDFNNMIDSKKITQLPLVAKYKLGASAVVAGPRFTGGDIIC 540
QY 541 TENGSAATIVYTPDVSYSKYRARIHYASTQITFTLSLDGAFPNQYFDKTIKNGDTLT 600
    |||
Dd 541 TENGSAATIVYTPDVSYSKYRARIHYASTQITFTLSLDGAFPNQYFDKTIKNGDTLT 600
QY 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIYPN 644
    |||
Dd 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIYPN 644

RESULT 21
AAW34815
ID AAW34815 standard; Protein; 644 AA.
XX
AC AAW34815;
XX
DT 25-FEB-1998 (first entry)
DE
XX Novel CryIIIA mutant protein D354A.
DE
XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
FH
XX
FT Key Location/Qualifiers
FT Misc-difference 354 /label= D354A
FT /note= "wild type Asp replaced with Ala"
XX
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLUBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Janssens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIIIA proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands

```

```

CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 8.31 microgram per millilitre, compared to 11.60 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA;
XX
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPNRSEHDTIKTTEENNEVPTNHQYPLAETPPTLEDLNKKEFLMTADNTEALDSS 60
Dd 1 MNPNRSEHDTIKTTEENNEVPTNHQYPLAETPPTLEDLNKKEFLMTADNTEALDSS 60
QY 61 TTQDVIQKISVGDILGVGFPPFGALVSYFTNFELNTIMPSDPMKAFMEQVADLMDOK 120
Dd 61 TTQDVIQKISVGDILGVGFPPFGALVSYFTNFELNTIMPSDPMKAFMEQVADLMDOK 120
QY 121 IADYAKNNKALAELOGLQNNVEDYVSALSMQKNVSSRNPSQGRIRLELSQAESHRNS 180
Dd 121 IADYAKNNKALAELOGLQNNVEDYVSALSMQKNVSSRNPSQGRIRLELSQAESHRNS 180
QY 181 MPSPRISGEVFLFTTYAQAANTHLFLKDAQIYGEEMGEKEDIAPFYRKQLTQEXT 240
Dd 181 MPSPRISGEVFLFTTYAQAANTHLFLKDAQIYGEEMGEKEDIAPFYRKQLTQEXT 240
QY 241 DHCKWYNVGDILKRGSSYSESWNFNRYRREMTLTVDLALPLVYRLYRREVTET 300
Dd 241 DHCKWYNVGDILKRGSSYSESWNFNRYRREMTLTVDLALPLVYRLYRREVTET 300
QY 301 RDVLTDPVGNVNNRGYGTFTFSNIENIRKPHLFEDYLRHQFTFRQPGYGGASFNWMS 360
Dd 301 RDVLTDPVGNVNNRGYGTFTFSNIENIRKPHLFEDYLRHQFTFRQPGYGGASFNWMS 360
QY 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Dd 361 GNVYSTRPSIGSNDITSPFYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
QY 421 KVEFSQVNDQTDASTQTYDSKRNKAVSWDSIDQLPETTDEPLEKGYSHQNLNVMCF 480
Dd 421 KVEFSQVNDQTDASTQTYDSKRNKAVSWDSIDQLPETTDEPLEKGYSHQNLNVMCF 480
QY 481 MGSRGITPVLWTHTKSVDFNNMIDSKKITQLPLVAKYKLGASAVVAGPRFTGGDIIC 540
Dd 481 MGSRGITPVLWTHTKSVDFNNMIDSKKITQLPLVAKYKLGASAVVAGPRFTGGDIIC 540
QY 541 TENGSAATIVYTPDVSYSKYRARIHYASTQITFTLSLDGAFPNQYFDKTIKNGDTLT 600
Dd 541 TENGSAATIVYTPDVSYSKYRARIHYASTQITFTLSLDGAFPNQYFDKTIKNGDTLT 600
QY 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIYPN 644
Dd 601 YNSFNLASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIYPN 644

RESULT 22
AAW34816
ID AAW34816 standard; Protein; 644 AA.
XX
XX
AC AAW34816;
XX
DT 25-FEB-1998 (first entry)
XX

```

Oy		181	MPSAISGEYELFTLTYYAAOANHTLFLTKAOIYGEEMGVEKEDIDAEFYRKOLKLQOEYI	240
Dd		181	MFSPAISGEYELFTLTYYAAOANHTLFLTKDQOITGEEMGETEKEDI AEFTRKOLKLQOEYT	240
Oy		241	DHCVKWYNVGLDKLRGSSYESWVNFRNRYRREBMTLTVDLLALFPLYDVRLYPKEVKTELT	300
Dd		241	DHCVKWYNVGLDKLRGSSYESWVNFRNRYRREMTLTVDLLALFPLYDVRLYPKEVKTELT	300
Oy		301	RDLVTDPVGVNNLRGYGTTFNSINENTIRKPHLFDYLHRIQGFHTRFGPYTGNDSEFNYS	360
Dd		301	RDLVTDPVGVNNLRGYGTTFNSINENTIRKPHLFDYLHRIQGFHTRFGPYTGNDSEFNYS	360
Oy		361	GNYSTRPSTISNDIIITSPFGNKSSPEPVONLEFNGEKEYRAVANNTMLAWPMSAVTSGVT	420
Dd		361	GNYSTRPSTISSNDIIITSPFGNKSSPEPVONLEFNGEKEYRAVAANTMLAWASAVTSGVT	420
Oy		421	KVESQYNDQJDEASTQTYDSKRNVGAVSMDSIDQLPETTDDBLEKGYSHQNLNVMCFL	480
Dd		421	KVESQYNDQJDEASTQTYDSKRNVGAVSMDSIDQLPETTDDBLEKGYSHQNLNVMCFL	480
Oy		481	MQGSRGITPLVTWTNHKSVDFFNMIDSKKITQLPLVKAAYKLQSCASVYAAGRFPGGDITOC	540
Dd		481	MQGSRGITPLVTWTNHKSVDFFNMIDSKKITQLPLVKAAYKLQSCASVYAAGRFPGGDITOC	540
Oy		541	TENGSAAITYTPPVVSYSOKYRARIHVASTSQITFTSLDGAPNOYYYFPKTIINKGDTLT	600
Dd		541	TENGSAAITYTPPDVSVTSQKTRAHIHASTSQITFTSLDGAPPNQOYIFPKTIINKGDTLT	600
Oy		601	YNSENLASFSTPFELSGNNLIQIGVTGLSAGDKYVIDKIEFIIPVN 644	
Dd		601	YNSENLASFSTPFELSGNNLIQIGVTGLSAGDKYVIDKIEFIIPVN 644	
RESULT_23				
AAMw34817		ID	AAMw34817 standard; protein; 644 AA.	
xx		AAMw34817:		
AC		25-FEB-1998	(first entry)	
xx				
DE			Novel CryIIIA mutant protein S413A.	
xx				
KW			cryIIIA gene; corn rootworm toxicity; CryIIIA protein;	
KW			increased toxicity; Coleopteran insect; Colorado potato beetle;	
KW			relative solvent accessibility; plant resistance;	
KX			Diabrotica virgifera virgifera.	
xx			Synthetic.	
OS			Bacillus thuringiensis.	
xx				
FH		Key	Location/Qualifiers	
FT		Misc-difference 413	/label= "S413A"	
FT			/note= "wild type Ser replaced with Ala"	
PX		US5659123-A.		
xx				
xx		19-AUG-1997.		
FD				
xx		26-AUG-1994;	94US-0295060.	
xx				
PR		26-AUG-1994;	94US-0295060.	
xx				
PA		(PLABZ) PLANT GENETIC SYSTEMS NY.		
PI		Jansens S. Peferoen M. Van Rie J;		
xx				
DR		WPJ; 1997-424316/39.		
PT			Modified Bacillus thuringiensis CryIII proteins - with increased	
			toxicity against insect pests, particularly Coleopteran insects,	

PT e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -: 22pp; English.

XX
CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of *Bacillus*
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards *Diabrotica*
CC *virgifera virgifera* was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 1.93 microgram per millilitre, compared to 5.55 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.

XX
SQ Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDITKTENNENVPFNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPFNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
OY 61 TTKDVIQKGISVVDLLGVGFPFGALVSFTYNFLTNPSEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQKGISVVDLLGVGFPFGALVSFTYNFLTNPSEDPKAFMEQVEALMDOK 120
OY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRITRELFQSAESHFRNS 180
DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRITRELFQSAESHFRNS 180
OY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRITRELFQSAESHFRNS 180
DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRITRELFQSAESHFRNS 180
OY 181 MPSEFASGEVLEFLTYAQAAMTHFLKDAQIYGEWGEKEDIAEFKROKLKTQOET 240
DB 181 MPSEFASGEVLEFLTYAQAAMTHFLKDAQIYGEWGEKEDIAEFKROKLKTQOET 240
OY 241 DHCVKNNYNGDLKLRGSSYESWVNFNRYRREMTLVLDLIAFPPLYDVALYKREKTELT 300
DB 241 DHCVKNNYNGDLKLRGSSYESWVNFNRYRREMTLVLDLIAFPPLYDVALYKREKTELT 300
OY 301 RDVLTPIYGVNNLRGTYGTFSSNIENYIRKPHLFDYLRHIOFTRNPQCYGNDSPFNWS 360
DB 301 RDVLTPIYGVNNLRGTYGTFSSNIENYIRKPHLFDYLRHIOFTRNPQCYGNDSPFNWS 360
OY 361 GNVSTRPISGNDITTSFYGKNSSEPVQNLFEENGKRYRAVANINLAWVPAAYSGVT 420
DB 361 GNVSTRPISGNDITTSFYGKNSSEPVQNLFEENGKRYRAVANINLAWVPAAYSGVT 420
OY 421 KVEFSQYNDQTEASTQYDYSKRNQAVSWDSIDQLPETTDEPLEKGYSHQNLVVMCFL 480
DB 421 KVEFSQYNDQTEASTQYDYSKRNQAVSWDSIDQLPETTDEPLEKGYSHQNLVVMCFL 480
OY 481 MGSRSRTIYVLVTHKSVFFNMIDSKITPOLPLVAKAYLOGASVAVGPRFTGGDIQC 540
DB 481 MGSRSRTIYVLVTHKSVFFNMIDSKITPOLPLVAKAYLOGASVAVGPRFTGGDIQC 540
OY 541 TENGSAATYVTPDVSYSQYRARIRHYASTSQTFTLSIDGAFPMQYFDKTIKNGDILT 600
DB 541 TENGSAATYVTPDVSYSQYRARIRHYASTSQTFTLSIDGAFPMQYFDKTIKNGDILT 600
OY 601 YNSFNLFASFTEPELSSGNLQIGVGLSAGDVKYIDKIEFIPVN 644
DB 601 YNSFNLFASFTEPELSSGNLQIGVGLSAGDVKYIDKIEFIPVN 644

RESULT 24

AAW34818
ID AAW34818 standard; Protein: 644 AA.

XX
AC AAW34818;

XX
DT 25-FEB-1998 (first entry)

XX
DE Novel CryIIIA mutant protein Q482A.

XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
XX *Diabrotica virgifera virgifera*.

OS Synthetic.
XX *Bacillus thuringiensis*.

XX
FH Key Location/Qualifiers
FT Misc-difference 482

FT /label="Q482A
FT /note="wild type Gln replaced with Ala"

XX
PN US659123-A.

XX
PD 19-AUG-1997.

XX
PP 26-AUG-1994; 94US-0295060.

XX
PR 26-AUG-1994; 94US-0295060.

XX
PA (PLBZ) PLANT GENETIC SYSTEMS NV.

XX
PI Jansens S, Peferoen M, Van Rie J;

XX
DR WPI: 1997-424316/39.

XX
PT Modified *Bacillus thuringiensis* CryIIIA proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle

XX
PS Example 1; Page -: 22pp; English.

XX
CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of *Bacillus*
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards *Diabrotica*
CC *virgifera virgifera* was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 1.96 microgram per millilitre, compared to 5.55 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.

XX
SQ Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDITKTENNENVPFNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPFNHVOYPLAETPNPTLEDLNKKEFLRMADNNTALDSS 60
OY 61 TTKDVIQKGISVVDLLGVGFPFGALVSFTYNFLTNPSEDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQKGISVVDLLGVGFPFGALVSFTYNFLTNPSEDPKAFMEQVEALMDOK 120

Db 61 TTKVDYIOKGISVGDLLGVGPFPGALVSPYTNFLNTIMPSEDDPKAFMEQVLEALMDQK 120
 QY 121 IADYAKNKALAELOGLOQNNVEDYVSALSSWQKNPVSSNPHSOGRIREFLSQASHEPRNS 180
 Db 121 IADYAKNKALAELOGLOQNNVEDYVSALSSWQKNPVSSNPHSOGRIREFLSQASHEPRNS 180
 QY 181 MPFAISGEVLEFLTTVAQAANTHFLFKDAQIYGEEMGKEDEIAEFYKROLKLTQET 240
 Db 181 MPFAISGEVLEFLTTVAQAANTHFLFKDAQIYGEEMGKEDEIAEFYKROLKLTQET 240
 QY 241 DHCVMYVNGDLKLGSSYESVWVNNRREMTLVLDLALFPLDYRLPKVEKTELT 300
 Db 241 DHCVMYVNGDLKLGSSYESVWVNNRREMTLVLDLALFPLDYRLPKVEKTELT 300
 QY 301 RDVLTDPVGVNMLRGYGTFSNENYTRKPHLFDYLRIOFHFRFGYGYGNDSPFNWS 360
 Db 301 RDVLTDPVGVNMLRGYGTFSNENYTRKPHLFDYLRIOFHFRFGYGYGNDSPFNWS 360
 QY 361 GNVSTRPSIGSNDITTSFPGNKSSEPVQNLFEFGKEVYRAVANTNLAVPMSAVYSGVT 420
 Db 361 GNVSTRPSIGSNDITTSFPGNKSSEPVQNLFEFGKEVYRAVANTNLAVPMSAVYSGVT 420
 QY 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPEPTDEPLEKGYSHQNLVYMCFL 480
 Db 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPEPTDEPLEKGYSHQNLVYMCFL 480
 QY 481 MGSRGITPVLTWTHKSVDFEKNMIDSKITQPLVKAKKLGSGASVAVGPRFTGGDIIOC 540
 Db 481 MGSRGITPVLTWTHKSVDFEKNMIDSKITQPLVKAKKLGSGASVAVGPRFTGGDIIOC 540
 QY 541 TENGSAATYVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFEDKTIKNGDILT 600
 Db 541 TENGSAATYVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFEDKTIKNGDILT 600
 QY 601 YNSFNLASFTPELISGNMIGVGLSAGDKVYIDKIEFIVN 644
 Db 601 YNSFNLASFTPELISGNMIGVGLSAGDKVYIDKIEFIVN 644
 RESULT 25
 AAW34819
 ID AAW34819 standard; Protein: 644 AA.
 AC AAW34819;
 DT 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein Q411A.
 KW cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH Key location/Qualifiers
 FT Misc-difference 411
 FT /label= Q411A
 FT /note= "Wild type Trp replaced with Ala"
 FT US5659123-A.
 PD 19-AUG-1997.
 PF 26-AUG-1994; 94US-0295060.
 PR 26-AUG-1994; 94US-0295060.
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX Jansens S, Peferoen M, Van Rie J;

XX WPI: 1997-424316/39.
 DR Modified Bacillus thuringiensis CryIII proteins - with increased
 XX toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 PT Claim 9: Page -: 22pp: English.
 PS Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be >243 microgram per millilitre, compared to 3.86 microgram per
 CC millilitre for the wild type CryIIIA protein. This mutant protein is
 CC recognised as a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 XX Sequence 644 AA:
 SQ
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNPNNRSEHDITKTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLMTADNNTALDSS 60
 Db 1 MNPNNRSEHDITKTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLMTADNNTALDSS 60
 QY 61 TTKVDYIOKGISVGDLLGVGPFPGALVSPYTNFLNTIMPSEDDPKAFMEQVLEALMDQK 120
 Db 61 TTKVDYIOKGISVGDLLGVGPFPGALVSPYTNFLNTIMPSEDDPKAFMEQVLEALMDQK 120
 QY 121 IADYAKNKALAELOGLOQNNVEDYVSALSSWQKNPVSSNPHSOGRIREFLSQASHEPRNS 180
 Db 121 IADYAKNKALAELOGLOQNNVEDYVSALSSWQKNPVSSNPHSOGRIREFLSQASHEPRNS 180
 QY 181 MPFAISGEVLEFLTTVAQAANTHFLFKDAQIYGEEMGKEDEIAEFYKROLKLTQET 240
 Db 181 MPFAISGEVLEFLTTVAQAANTHFLFKDAQIYGEEMGKEDEIAEFYKROLKLTQET 240
 QY 241 DHCVMYVNGDLKLGSSYESVWVNNRREMTLVLDLALFPLDYRLPKVEKTELT 300
 Db 241 DHCVMYVNGDLKLGSSYESVWVNNRREMTLVLDLALFPLDYRLPKVEKTELT 300
 QY 301 RDVLTDPVGVNMLRGYGTFSNENYTRKPHLFDYLRIOFHFRFGYGYGNDSPFNWS 360
 Db 301 RDVLTDPVGVNMLRGYGTFSNENYTRKPHLFDYLRIOFHFRFGYGYGNDSPFNWS 360
 QY 361 GNVSTRPSIGSNDITTSFPGNKSSEPVQNLFEFGKEVYRAVANTNLAVPMSAVYSGVT 420
 Db 361 GNVSTRPSIGSNDITTSFPGNKSSEPVQNLFEFGKEVYRAVANTNLAVPMSAVYSGVT 420
 QY 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPEPTDEPLEKGYSHQNLVYMCFL 480
 Db 421 KVEFSQYNDQDEASTQYDYSKRNVGAVSWDSIDLPEPTDEPLEKGYSHQNLVYMCFL 480
 QY 481 MGSRGITPVLTWTHKSVDFEKNMIDSKITQPLVKAKKLGSGASVAVGPRFTGGDIIOC 540
 Db 481 MGSRGITPVLTWTHKSVDFEKNMIDSKITQPLVKAKKLGSGASVAVGPRFTGGDIIOC 540
 QY 541 TENGSAATYVTPDVYSOKYRARIHYASTSQITFTLSLDGAPFNQYFEDKTIKNGDILT 600

```

|||||
Db 541 TENGSAATITVTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDILT 600
QY 601 YNSFNLASSTPEPESGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 601 YNSFNLASSTPEPESGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 26
AAW34820
ID AAW34820 standard: Protein: 644 AA.
XX
AC AAW34820:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein T406A.
XX
KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
KM increased toxicity; Coleopteran insect; Colorado potato beetle;
KM relative solvent accessibility; plant resistance;
KM Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 406 /label= T406A
FT /note= "wild type Thr replaced with Ala"
FT
FT
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI: 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW3481-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX and can be used to combat, or improve plant resistance towards insects.
XX Specifically, the toxicity of the present sequence towards Diabrotica
XX virgifera virgifera was tested. The EC50 value (concentration at which
XX 50% feeding inhibition is observed) of the present protein was found to
XX be 5.50 microgram per millilitre, compared to 2.42 microgram per
XX millilitre for the wild type CryIIIA protein.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 644 AA:
XX
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;

```

```

Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDTIKTTENNENVEPTNHVQYPLAETPPTLEDLNYKEEFLMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTTENNENVEPTNHVQYPLAETPPTLEDLNYKEEFLMTADNNTALDSS 60
QY 61 TTKDVIQKGISVVDLLGVVGFPPGALVSEFTYTNFLMTIPSEDPMKAFMEQVEALMDCK 120
Db 61 TTKDVIQKGISVVDLLGVVGFPPGALVSEFTYTNFLMTIPSEDPMKAFMEQVEALMDCK 120
QY 121 IADYAKKKALAELOGLONNEDYVSALSSWQKPNVSSRNPHSGRIRELPSQAESHPRNS 180
Db 121 IADYAKKKALAELOGLONNEDYVSALSSWQKPNVSSRNPHSGRIRELPSQAESHPRNS 180
QY 181 MPEFAISGEVLEFLTYTAQANTHLEFLKDAQIYGEEMGYEKDIAEFKKRQDLQOEXT 240
Db 181 MPEFAISGEVLEFLTYTAQANTHLEFLKDAQIYGEEMGYEKDIAEFKKRQDLQOEXT 240
QY 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPPLVDVRLYREXVTELT 300
Db 241 DHCKWYNVGLDKLRGSSYSWVNFNRYRREMTLVLDLALPPLVDVRLYREXVTELT 300
QY 301 RDVLTDPVGVNMLRGYGTTFNSIENYIRKPHLEFDYLRHQFTTRPOPGYGGNDSFNYS 360
Db 301 RDVLTDPVGVNMLRGYGTTFNSIENYIRKPHLEFDYLRHQFTTRPOPGYGGNDSFNYS 360
QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSDPVONLEFNKEKYRAVANNTLAWPSAVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPFYGNKSSDPVONLEFNKEKYRAVANNTLAWPSAVYSGVT 420
QY 421 KVEFSQYNDQTDASTQOTVYSKRNKGVASWDSIDOLPPEPTDPELEKGSQOLNTYMCFL 480
Db 421 KVEFSQYNDQTDASTQOTVYSKRNKGVASWDSIDOLPPEPTDPELEKGSQOLNTYMCFL 480
QY 481 MGSRCGTIPVLTWTHKSVDFEFNMIDSKITQPLVAVAYKLQSGASVYAPRFTGDDIIOC 540
Db 481 MGSRCGTIPVLTWTHKSVDFEFNMIDSKITQPLVAVAYKLQSGASVYAPRFTGDDIIOC 540
QY 541 TENGSAATITVTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDILT 600
Db 541 TENGSAATITVTPDVSYSKYRARIHYASTQITFTLSLDGAPFNQYFDKTIKNGDILT 600
QY 601 YNSFNLASSTPEPESGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 601 YNSFNLASSTPEPESGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 27
AAW34821
ID AAW34821 standard: Protein: 644 AA.
XX
AC AAW34821:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein G349A.
XX
XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX increased toxicity; Coleopteran insect; Colorado potato beetle;
XX relative solvent accessibility; plant resistance;
XX Diabrotica virgifera virgifera.
XX
XX Synthetic.
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 349 /label= G349A
FT /note= "wild type Gly replaced with Ala"
FT
FT
XX
XX US5659123-A.
XX
XX 19-AUG-1997.

```

XX 26-AUG-1994; 94US-0295060.
 PF
 XX 26-AUG-1994; 94US-0295060.
 PR
 XX (PLB2) PLANT GENETIC SYSTEMS NV.
 PA
 XX Jansens S, Peferoen M, Van Rie J;
 PI
 XX WPI: 1997-424316/39.
 DR
 XX
 PT Modified Bacillus thuringiensis CryIIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Claim 9; Page -: 22pp; English.
 XX
 CC Novel CryIIII proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIII protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIII proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be >243 microgram per millilitre, compared to 2.42 microgram per
 CC millilitre for the wild type CryIIII protein. This mutant protein is
 CC recognised as a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIII protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 CC
 XX Sequence 644 AA:
 SO
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 MNPNNRSHDITKTENNENPNNHVOYPLAETPNPTLEDLKYKELRMTAANNTEALDSS 60
 Db 1 MNPNNRSHDITKTENNENPNNHVOYPLAETPNPTLEDLKYKELRMTAANNTEALDSS 60
 Oy 61 TTKDVIOGCISSVGDLLGVGFPGALVSYFTNPLNTIMPSEDPMKAFMEQVEALMDQK 120
 Db 61 TTKDVIOGCISSVGDLLGVGFPGALVSYFTNPLNTIMPSEDPMKAFMEQVEALMDQK 120
 Oy 121 IADYAKKNALELOGLQNNVEDYVSALLSWOKNPVSSNPHSOGRIREFLSQASHFRNS 180
 Db 121 IADYAKKNALELOGLQNNVEDYVSALLSWOKNPVSSNPHSOGRIREFLSQASHFRNS 180
 Oy 181 MSPFAISGEVLEFTTYAOAANTHLEFLKDAOIYGEEMGYEKEDIAEYKRSQKLTOCYT 240
 Db 181 MSPFAISGEVLEFTTYAOAANTHLEFLKDAOIYGEEMGYEKEDIAEYKRSQKLTOCYT 240
 Oy 241 DHCVMYVNGDLKLGSSYESVWVNNRRYREMTLVLDLALFLPYDRALKPEKKEKELT 300
 Db 241 DHCVMYVNGDLKLGSSYESVWVNNRRYREMTLVLDLALFLPYDRALKPEKKEKELT 300
 Oy 301 RDVLTDPYGVNMLRGYITTSNLENTYRKPHLPDYLRHRIOPHRFQPAYYGNDSFNWMS 360
 Db 301 RDVLTDPYGVNMLRGYITTSNLENTYRKPHLPDYLRHRIOPHRFQPAYYGNDSFNWMS 360
 Oy 361 GMYVSTRSISGNDITITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAWPSAVYSGVT 420
 Db 361 GMYVSTRSISGNDITITSPFYGNKSSEPVONLEFNGEKVYRAVANTNLAWPSAVYSGVT 420
 Oy 421 KVEFSQYNDQTDASTQTYDSKRNNGAVSWDSIDQLPETTDEPLEKGYSHQLNVMCFL 480

Db 421 KVEFSQYNDQTDASTQTYDSKRNNGAVSWDSIDQLPETTDEPLEKGYSHQLNVMCFL 480
 Oy 481 MOGSRGTIPVLTWTHKSVDFENMIDSKKITQPLVNAVYKLOSGASVVAAPRTGGDIIOC 540
 Db 481 MOGSRGTIPVLTWTHKSVDFENMIDSKKITQPLVNAVYKLOSGASVVAAPRTGGDIIOC 540
 Oy 541 TENGSAATIVTPDVSVSGKRYRARIHYASTSQITFTLSLDGAPFNQYFDKTIINKGDTLT 600
 Db 541 TENGSAATIVTPDVSVSGKRYRARIHYASTSQITFTLSLDGAPFNQYFDKTIINKGDTLT 600
 Oy 601 YNSFNLASFSTPELISGNMLQIGVTGLSAGDKVYIDKIEFTIPVN 644
 Db 601 YNSFNLASFSTPELISGNMLQIGVTGLSAGDKVYIDKIEFTIPVN 644
 RESULT 28
 AAW34822
 ID AAW34822 standard; Protein; 644 AA.
 XX
 AC AAW34822;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIII mutant protein V311A.
 XX
 KW CryIIII gene: corn rootworm toxicity; CryIIII protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 311
 FT /label= V311A
 FT /note= "wild type Val replaced with Ala"
 XX
 PN US5659123-A.
 XX
 PD 19-AUG-1997.
 XX
 PF 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 XX
 PI Jansens S, Peferoen M, Van Rie J;
 XX
 DR WPI: 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1; Page -: 22pp; English.
 XX
 CC Novel CryIIII proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIII protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIII proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.09 microgram per millilitre, compared to 1.21 microgram per

CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

SQ Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNSEHDITKTENNENVPYTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
 DB 1 MNPNNSEHDITKTENNENVPYTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
 QY 61 TTKDVIQKGISVVGDLGIVGVPFGGALVSFTYNTLWTPSEDPKAMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVGDLGIVGVPFGGALVSFTYNTLWTPSEDPKAMEQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRRELSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRRELSQASHFRNS 180
 QY 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
 DB 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
 QY 241 DHCVKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDIALFPLDYRLYKPKETELT 300
 DB 241 DHCVKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDIALFPLDYRLYKPKETELT 300
 QY 301 RDVLTDPYIVGVNMLRGYGTTFNSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYS 360
 DB 301 RDVLTDPYIVGVNMLRGYGTTFNSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYS 360
 QY 361 GNVVSRPISGNDITTSFYGNKSEPEYQNLFEFGKRYAVANTNLAWPSAVYSYVT 420
 DB 361 GNVVSRPISGNDITTSFYGNKSEPEYQNLFEFGKRYAVANTNLAWPSAVYSYVT 420
 QY 421 KYEFSQYNDQDEASTQYTDKSRNGAVSMDSDIDLPETDEPLEKGYSHOANVMCFU 480
 DB 421 KYEFSQYNDQDEASTQYTDKSRNGAVSMDSDIDLPETDEPLEKGYSHOANVMCFU 480
 QY 481 MGSGRGTIVLTWTHKSVDFENMIDSKITQLPLVKAAYKLOSGASVAGPRETGGDITQC 540
 DB 481 MGSGRGTIVLTWTHKSVDFENMIDSKITQLPLVKAAYKLOSGASVAGPRETGGDITQC 540
 QY 541 TENGSAATYVTPDVSYSQYRARIHYASTQITFTLSIDGAPFNOYQYEDKTINKGDTLT 600
 DB 541 TENGSAATYVTPDVSYSQYRARIHYASTQITFTLSIDGAPFNOYQYEDKTINKGDTLT 600
 QY 601 YNSFNLASFPPELSGNNLQIGVGLSAGDKVYIDKIEFIIPVN 644
 DB 601 YNSFNLASFPPELSGNNLQIGVGLSAGDKVYIDKIEFIIPVN 644

RESULT 29
 AAM34823
 ID AAM34823 standard; Protein: 644 AA.
 XX
 AC AAM34823;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein N312A.
 XX
 KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX

FF Key Location/Qualifiers
 FF Misc-difference 312
 FT /label= N312A
 FT /note= "wild type Asn replaced with Ala"

US5659123-A.
 19-AUG-1997.
 26-AUG-1994; 94US-0295060.
 26-AUG-1994; 94US-0295060.
 (PLBZ) PLANT GENETIC SYSTEMS NV.
 Janssens S, Peferoen M, Van Rie J;
 WPI: 1997-424316/39.
 Modified Bacillus thuringiensis CryIII proteins - with increased
 toxicity against insect pests, particularly Coleopteran insects,
 e.g. corn rootworm and Colorado potato beetle
 Example 1; Page -: 22pp; English.

CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.65 microgram per millilitre, compared to 1.21 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

SQ Sequence 644 AA:
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNSEHDITKTENNENVPYTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
 DB 1 MNPNNSEHDITKTENNENVPYTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
 QY 61 TTKDVIQKGISVVGDLGIVGVPFGGALVSFTYNTLWTPSEDPKAMEQVEALMDOK 120
 DB 61 TTKDVIQKGISVVGDLGIVGVPFGGALVSFTYNTLWTPSEDPKAMEQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRRELSQASHFRNS 180
 DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRRELSQASHFRNS 180
 QY 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
 DB 181 MPSFAISGEVLEFLTYAQAANTHLFLKDAQIYGEWGEKEDIAEFYKROLKLTQEXT 240
 QY 241 DHCVKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDIALFPLDYRLYKPKETELT 300
 DB 241 DHCVKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDIALFPLDYRLYKPKETELT 300
 QY 301 RDVLTDPYIVGVNMLRGYGTTFNSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYS 360
 DB 301 RDVLTDPYIVGVNMLRGYGTTFNSNIENYIRKPHLFYDLHRIOFHTROPQGYGNDSPNYS 360

QY 361 GNYVSTRPSIGSNDITTSPEYGNKSSSEPVONLEFNGEKYRAVANNTNLAVPSPAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITTSPEYGNKSSSEPVONLEFNGEKYRAVANNTNLAVPSPAVYSGVT 420
 QY 421 KYEFQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 DB 421 KYEFQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 QY 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVKAYKLGSGASVYAGPRTGGDIQC 540
 DB 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVKAYKLGSGASVYAGPRTGGDIQC 540
 QY 541 TENGSAATITTYTPDYYSQYKRRARHYASTQITFTSLDAPFQYQYFEDTINKGDTLT 600
 DB 541 TENGSAATITTYTPDYYSQYKRRARHYASTQITFTSLDAPFQYQYFEDTINKGDTLT 600
 QY 601 YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 30
 AAM34824
 ID AAM34824 standard; Protein: 644 AA.
 XX
 AC AAM34824;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein N326A.
 XX
 KM cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 326
 FT /label= N326A
 FT /note="Wild type Asn replaced with Ala"
 FT
 FT US5659123-A.
 PN 19-AUG-1997.
 PD 26-AUG-1994; 94US-0295060.
 PF 26-AUG-1994; 94US-0295060.
 PR 26-AUG-1994; 94US-0295060.
 XX (PLB2) PLANT GENETIC SYSTEMS NV.
 PA
 PA Jansens S, Peferoen M, Van Rie J;
 PI WPI: 1997-424316/39.
 DR
 XX Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 PS Example 1: Page -: 22pp; English.
 XX
 CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 7.80 microgram per millilitre, compared to 2.40 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX
 SQ Sequence 644 AA;
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNEVPNTNHVQYPLAETPPTLEDLNTYKEFLBMTADNNTALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPNTNHVQYPLAETPPTLEDLNTYKEFLBMTADNNTALDSS 60
 QY 61 TTQVIOKGISVVDLLGVVGFPEFGALVSFYTNFLTNTIMPSEDPMKAFMEQVEALMDQK 120
 DB 61 TTQVIOKGISVVDLLGVVGFPEFGALVSFYTNFLTNTIMPSEDPMKAFMEQVEALMDQK 120
 QY 121 IADYAKKKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHRNS 180
 DB 121 IADYAKKKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSOGRIREFLSQAESHRNS 180
 QY 181 MPSPRISGEVLEFLTTTAAQAAANTHLFLKDAQYIGEMQYKEDIAEFYRQKLQOEY 240
 DB 181 MPSPRISGEVLEFLTTTAAQAAANTHLFLKDAQYIGEMQYKEDIAEFYRQKLQOEY 240
 QY 241 DHCKWYVWGLDKRGSSYESWVNFNRRREMTLTVDLALPFLYDVRLYPREVKTEL 300
 DB 241 DHCKWYVWGLDKRGSSYESWVNFNRRREMTLTVDLALPFLYDVRLYPREVKTEL 300
 QY 301 RDVLTDPITVGVNNLRGYGTTFNSIENYIRKPHLFDYLAHRIOPHTRFQPGYGNDSFNWMS 360
 DB 301 RDVLTDPITVGVNNLRGYGTTFNSIENYIRKPHLFDYLAHRIOPHTRFQPGYGNDSFNWMS 360
 QY 361 GNYVSTRPSIGSNDITTSPEYGNKSSSEPVONLEFNGEKYRAVANNTNLAVPSPAVYSGVT 420
 DB 361 GNYVSTRPSIGSNDITTSPEYGNKSSSEPVONLEFNGEKYRAVANNTNLAVPSPAVYSGVT 420
 QY 421 KYEFQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 DB 421 KYEFQYNDQDEASTQYTDKSRNKGAVSMDSIDOLPETTDEPLEKGYSHQLVVMCF 480
 QY 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVKAYKLGSGASVYAGPRTGGDIQC 540
 DB 481 MGSRGITPVLWTWTHKSVDFNMIDSKKITQLPLVKAYKLGSGASVYAGPRTGGDIQC 540
 QY 541 TENGSAATITTYTPDYYSQYKRRARHYASTQITFTSLDAPFQYQYFEDTINKGDTLT 600
 DB 541 TENGSAATITTYTPDYYSQYKRRARHYASTQITFTSLDAPFQYQYFEDTINKGDTLT 600
 QY 601 YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 31
 AAM34825
 ID AAM34825 standard; Protein: 644 AA.
 XX
 AC AAM34825;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein E387A.
 XX
 KM cryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;

```

KM Diabrotica virgifera virgifera.
XX Synthetic.
OS Bacillus thuringiensis.
XX
XX
FH Key Location/Qualifiers
FT MISC-difference 387
FT /Label= E387A
FT /note= "wild type Glu replaced with Ala"
XX
XX US5659123-A.
XX
XX 19-AUG-1997.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX 26-AUG-1994; 94US-0295060.
XX
XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX
XX Jansens S, Peferoen M, Van Rie J;
XX
XX WPI; 1997-424316/39.
XX
XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX Example 1; Page -: 22pp; English.
XX
XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands
XX directed towards or located at the molecular apex. The substituted amino
XX acids have a relative solvent accessibility of at least 40%, or are a
XX maximum distance of 3 amino acids away from an amino acid having at least
XX 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX and can be used to combat, or improve plant resistance towards insects.
XX Specifically, the toxicity of the present sequence towards Diabrotica
XX virgifera virgifera was tested. The EC50 value (concentration at which
XX 50% feeding inhibition is observed) of the present protein was found to
XX be 7.80 microgram per millilitre, compared to 2.40 microgram per
XX millilitre for the wild type CryIIIA protein.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 644 AA;
XX
XX Query Match 84.3%; Score 543; DB 18; Length 644;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MNPNNRESEHTPTIKTENNEVPNTNVOYPLAETPNPLEDNTYKEFLRMADNNTALDSS 60
XX DB 1 MNPNNRESEHTPTIKTENNEVPNTNVOYPLAETPNPLEDNTYKEFLRMADNNTALDSS 60
XX
XX 61 TTKDVIOKGISVVDLLGVGFPGGALVSFTNFLTNTIPSEDPKAKMEQVEALMDOK 120
XX DB 61 TTKDVIOKGISVVDLLGVGFPGGALVSFTNFLTNTIPSEDPKAKMEQVEALMDOK 120
XX
XX 121 IADYAKKAKALAELOGLONNEDYVSALSSQKPNVSSRNPHSGRIRELFSSQASHFRNS 180
XX DB 121 IADYAKKAKALAELOGLONNEDYVSALSSQKPNVSSRNPHSGRIRELFSSQASHFRNS 180
XX
XX 181 MPEFASISGVEVLELTYYAQAANTHFLFKDAQIYGEWGEKEDIKAEFKROLKLTQEXT 240
XX DB 181 MPEFASISGVEVLELTYYAQAANTHFLFKDAQIYGEWGEKEDIKAEFKROLKLTQEXT 240
XX
XX 241 DHCVKATYNGGLDKLRSSSVESWVNNRRYRREMTLVLDLIALFPLVDVRLYREKVTETLT 300
XX DB 241 DHCVKATYNGGLDKLRSSSVESWVNNRRYRREMTLVLDLIALFPLVDVRLYREKVTETLT 300
XX
XX 241 DHCVKATYNGGLDKLRSSSVESWVNNRRYRREMTLVLDLIALFPLVDVRLYREKVTETLT 300

```

```

XX 301 RDVLDPDIVGVNMLRGYGTFFSNIENYIRKPHLEFDYLHRIQFTRFQPGYRGDNSEFNYS 360
XX DB 301 RDVLDPDIVGVNMLRGYGTFFSNIENYIRKPHLEFDYLHRIQFTRFQPGYRGDNSEFNYS 360
XX
XX 361 GNYSTRPSGSNDITISPFYGNKSSPEPVONLENGSKYRAVANINLAWPSAVYSGVT 420
XX DB 361 GNYSTRPSGSNDITISPFYGNKSSPEPVONLENGSKYRAVANINLAWPSAVYSGVT 420
XX
XX 421 KVEFSQYNDQDEASTQYDSKRNVAWSIDQLPPEPTDDEPLEKGSYHOLNMYWCF 480
XX DB 421 KVEFSQYNDQDEASTQYDSKRNVAWSIDQLPPEPTDDEPLEKGSYHOLNMYWCF 480
XX
XX 481 MGSRGITIPVLTWTHKSVDFPNMIDSKKITQLPLVAYKQLQSGASVAVAGPRFTGDIIC 540
XX DB 481 MGSRGITIPVLTWTHKSVDFPNMIDSKKITQLPLVAYKQLQSGASVAVAGPRFTGDIIC 540
XX
XX 541 TENGSAAITVTPDVVSQKRYRARIHASTQITFLSLDGAFFNQYEDKTIKNGDTLT 600
XX DB 541 TENGSAAITVTPDVVSQKRYRARIHASTQITFLSLDGAFFNQYEDKTIKNGDTLT 600
XX
XX 601 YNSFNLFASFSTPELSCNNLQIGVTGLSAGDKYIYDKIEFIPVN 644
XX DB 601 YNSFNLFASFSTPELSCNNLQIGVTGLSAGDKYIYDKIEFIPVN 644
XX
XX RESULT 32
XX AAW34826
XX ID AAW34826 standard; Protein; 644 AA.
XX
XX AC AAW34826;
XX
XX DT 25-FEB-1998 (first entry)
XX
XX XX Novel CryIIIA mutant protein K384A.
XX
XX KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX increased toxicity; Coleopteran insect; Colorado potato beetle;
XX relative solvent accessibility; plant resistance;
XX Diabrotica virgifera virgifera.
XX
XX OS Synthetic.
XX
XX XX Bacillus thuringiensis.
XX
XX FH Key Location/Qualifiers
XX FT MISC-difference 384
XX FT /Label= K384A
XX FT /note= "wild type Lys replaced with Ala"
XX
XX XX
XX XX US5659123-A.
XX XX
XX XX 19-AUG-1997.
XX XX
XX XX 26-AUG-1994; 94US-0295060.
XX XX
XX XX 26-AUG-1994; 94US-0295060.
XX XX
XX XX (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX XX
XX XX Jansens S, Peferoen M, Van Rie J;
XX XX
XX XX WPI; 1997-424316/39.
XX XX
XX XX Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
XX XX Example 1; Page -: 22pp; English.
XX XX
XX XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
XX mutagenesis of domain II of the CryIIIA protein of Bacillus
XX thuringiensis. All the positions changed to alanine in these proteins
XX are located in some of the solvent exposed loops and beta-strands

```

CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 1.32 microgram per millilitre, compared to 2.88 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

CC Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNEVPNNHQQYPLAETPNPTLEDLNYKKEFLRMTADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNEVPNNHQQYPLAETPNPTLEDLNYKKEFLRMTADNNTALDSS 60
 QY 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIMPSEDPWKAFMQVEALMDQK 120
 DB 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIMPSEDPWKAFMQVEALMDQK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPVSSRNPHSQGRIRLFQSAESHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPVSSRNPHSQGRIRLFQSAESHFRNS 180
 QY 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLQLTOEYT 240
 DB 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLQLTOEYT 240
 QY 241 DHCVKYVNGDLKLRSSYESVWNEFRYRREMTLVLDLAFPLDYVALYKREKTELT 300
 DB 241 DHCVKYVNGDLKLRSSYESVWNEFRYRREMTLVLDLAFPLDYVALYKREKTELT 300
 QY 301 RDVLDPYGVNNLKGTYGTFSTNIENYIRKPHFLDYLRIQPHTRPQPGYGNDSFNWS 360
 DB 301 RDVLDPYGVNNLKGTYGTFSTNIENYIRKPHFLDYLRIQPHTRPQPGYGNDSFNWS 360
 QY 361 GNVSRRPSIGSNDITTSFYGNKSEPVQNLFEENGEXYRAVANNTLAWPSAYISGYT 420
 DB 361 GNVSRRPSIGSNDITTSFYGNKSEPVQNLFEENGEXYRAVANNTLAWPSAYISGYT 420
 QY 421 KVEFSQYNDQDEASTQYDYSKRNKGVASVMSIDQLPETTDEPLEKGYSHQLNVMCFL 480
 DB 421 KVEFSQYNDQDEASTQYDYSKRNKGVASVMSIDQLPETTDEPLEKGYSHQLNVMCFL 480
 QY 481 MGSRRITIVLTTHKSVDFPNKIDSKITQPLVAVAYKLGASAVVAAPRTGGDIIOC 540
 DB 481 MGSRRITIVLTTHKSVDFPNKIDSKITQPLVAVAYKLGASAVVAAPRTGGDIIOC 540
 QY 541 TENGSAATIVYPPDVYSOKYRARIHYASTSQTFTLSLDGAPFNQYDFDKTINKGDTLT 600
 DB 541 TENGSAATIVYPPDVYSOKYRARIHYASTSQTFTLSLDGAPFNQYDFDKTINKGDTLT 600
 QY 601 YNSFNLAASFSTPELSGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLAASFSTPELSGNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 33

AAW34827 standard; Protein; 644 AA.

AAW34827;

25-FEB-1998 (first entry)

XX

DE Novel CryIIIA mutant protein S385A.

XX CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.

OS Synthetic.
 OS Bacillus thuringiensis.

FH Key Location/Qualifiers

FT MISC-difference 385 /label= S385A

FT /note= "wild type Ser replaced with Ala"

PN US5659123-A.

PD 19-AUG-1997.

PE 26-AUG-1994; 94US-0295060.

PF 26-AUG-1994; 94US-0295060.

PR (PLBZ) PLANT GENETIC SYSTEMS NV.

PI Janssens S, Peferoen M, Van Rie J;

PS WPI: 1997-424316/39.

PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

XX Example 1: Page -: 22pp; English.

XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 0.78 microgram per millilitre, compared to 2.88 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

SO Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDITKTENNEVPNNHQQYPLAETPNPTLEDLNYKKEFLRMTADNNTALDSS 60
 DB 1 MNPNNRSEHDITKTENNEVPNNHQQYPLAETPNPTLEDLNYKKEFLRMTADNNTALDSS 60
 QY 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIMPSEDPWKAFMQVEALMDQK 120
 DB 61 TTKDVIQKGISVYGDLLGVGFPFGALVSFTYNTLNTIMPSEDPWKAFMQVEALMDQK 120
 QY 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPVSSRNPHSQGRIRLFQSAESHFRNS 180
 DB 121 IADYAKNKALAELOGLQNNVEDYVSSALSSWQKNPVSSRNPHSQGRIRLFQSAESHFRNS 180
 QY 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLQLTOEYT 240
 DB 181 MSFALSGEVEFLTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFKRLQLTOEYT 240

```

Db 181 MPEFAISGEVLELTYYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROKLKLTQEXT 240
Oy 241 DHCVKWYNNVGLDKRGSSYESWVNFRRYREMTLYLDIALPPLYDVRLYREKVTETLT 300
Db 241 DHCVKWYNNVGLDKRGSSYESWVNFRRYREMTLYLDIALPPLYDVRLYREKVTETLT 300
Oy 301 RDVLTDPVGVNNLRGCTGFESNIENYIRKPHLFDYLRHQFTFRPQPGYGNDSFNYS 360
Db 301 RDVLTDPVGVNNLRGCTGFESNIENYIRKPHLFDYLRHQFTFRPQPGYGNDSFNYS 360
Oy 361 GNVYSTRPSIGSNDIITSPYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Db 361 GNVYSTRPSIGSNDIITSPYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Oy 421 KVEFSQYNDQTDASTQYIDSKRNVAWSIDQLPPTTDEPLEKGSYHOLNVMCF 480
Db 421 KVEFSQYNDQTDASTQYIDSKRNVAWSIDQLPPTTDEPLEKGSYHOLNVMCF 480
Oy 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIQC 540
Db 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIQC 540
Oy 541 TENGSAATYVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Db 541 TENGSAATYVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Oy 601 YNSFNLASFTPELISGNLQIGVTGLSAGDKVYIDKIEFIPIVN 644
Db 601 YNSFNLASFTPELISGNLQIGVTGLSAGDKVYIDKIEFIPIVN 644

RESULT 34
AAW34828
ID AAW34828 standard; Protein: 644 AA.
XX
AC AAW34828;
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein V448A.
XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Dldbrotica virgifer a virgifer a.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FT Key Location/Qualifiers
FT MISC-difference 448 /label= V448A
FT /note= "wild type Val replaced with Ala"

US5659123-A.
XX
PD 19-AUG-1997.
XX
PE 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI Jansens S, Peferoen M, Van Rie J;
XX
DR WPI; 1997-424316/39.
XX
PT Modified Bacillus thuringiensis CryIIIA proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
PT e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -; 22pp; English.

```

```

XX
CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifer a virgifer a was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 11.52 microgram per millilitre, compared to 4.04 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA;
Query Match 84.3%; Score 543; DB 18; Length 644;
Best local similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 MNPNNRSEHDITKTENNEVPNTNHOYPLAETPPTLEDNLYKEFLMTADNTEALDSS 60
Db 1 MNPNNRSEHDITKTENNEVPNTNHOYPLAETPPTLEDNLYKEFLMTADNTEALDSS 60
Oy 61 TTKVDVIOKGISVVDLGGVGFPGGALVSFTYNFLNTIPSDPMPKAFMEQVEALMDOK 120
Db 61 TTKVDVIOKGISVVDLGGVGFPGGALVSFTYNFLNTIPSDPMPKAFMEQVEALMDOK 120
Oy 121 IADYAKKALAELOGLONNVEDYVYALSQKNPVSSRNPHSGGRITRELFQASHFRNS 180
Db 121 IADYAKKALAELOGLONNVEDYVYALSQKNPVSSRNPHSGGRITRELFQASHFRNS 180
Oy 181 MPEFAISGEVLELTYYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROKLKLTQEXT 240
Db 181 MPEFAISGEVLELTYYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROKLKLTQEXT 240
Oy 241 DHCVKWYNNVGLDKRGSSYESWVNFRRYREMTLYLDIALPPLYDVRLYREKVTETLT 300
Db 241 DHCVKWYNNVGLDKRGSSYESWVNFRRYREMTLYLDIALPPLYDVRLYREKVTETLT 300
Oy 301 RDVLTDPVGVNNLRGCTGFESNIENYIRKPHLFDYLRHQFTFRPQPGYGNDSFNYS 360
Db 301 RDVLTDPVGVNNLRGCTGFESNIENYIRKPHLFDYLRHQFTFRPQPGYGNDSFNYS 360
Oy 361 GNVYSTRPSIGSNDIITSPYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Db 361 GNVYSTRPSIGSNDIITSPYGNKSSPEVONLEFNGEKYRAVANINLAWPSAVYSGVT 420
Oy 421 KVEFSQYNDQTDASTQYIDSKRNVAWSIDQLPPTTDEPLEKGSYHOLNVMCF 480
Db 421 KVEFSQYNDQTDASTQYIDSKRNVAWSIDQLPPTTDEPLEKGSYHOLNVMCF 480
Oy 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIQC 540
Db 481 MGSRGITPVLTWTHKSVDFNMIDSKITQLPLVKAAYKLGASAVVAGPRTGGDIQC 540
Oy 541 TENGSAATYVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Db 541 TENGSAATYVTPDVYSQKRYRARIHYASTQTITFLSDGAPFNQYFDKTIKNGDTLT 600
Oy 601 YNSFNLASFTPELISGNLQIGVTGLSAGDKVYIDKIEFIPIVN 644
Db 601 YNSFNLASFTPELISGNLQIGVTGLSAGDKVYIDKIEFIPIVN 644

RESULT 35
AAW34829
ID AAW34829 standard; Protein: 644 AA.

```

```

XX AC AAM34829;
XX DT 25-FEB-1998 (first entry)
XX DE Novel CryIIIA mutant protein S449A.
XX KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX KM increased toxicity; Coleopteran insect; Colorado potato beetle;
XX KM relative solvent accessibility; plant resistance;
XX KM Diabrotica virgifera virgifera.
XX OS Synthetic.
XX OS Bacillus thuringiensis.
XX FT Key Location/Qualifiers
XX FT Misc-difference 449 /label= S449A
XX FT /note= "wild type Ser replaced with Ala"
XX PN US5659123-A.
XX PD 19-AUG-1997.
XX PE 26-AUG-1994; 94US-0295060.
XX PR 26-AUG-1994; 94US-0295060.
XX PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX PI Jansens S, Peferoen M, Van Rie J;
XX DR WPI: 1997-424316/39.
XX PT Modified Bacillus thuringiensis CryIII proteins - with increased
XX PT toxicity against insect pests, particularly Coleopteran insects,
XX PT e.g. corn rootworm and Colorado potato beetle
XX PS Example 1; Page -: 22pp; English.
XX CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
XX CC mutagenesis of domain II of the CryIIIA protein of Bacillus
XX CC thuringiensis. All the positions changed to alanine in these proteins
XX CC are located in some of the solvent exposed loops and beta-strands
XX CC directed towards or located at the molecular apex. The substituted amino
XX CC acids have a relative solvent accessibility of at least 40%, or are a
XX CC maximum distance of 3 amino acids away from an amino acid having at least
XX CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
XX CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
XX CC and can be used to combat, or improve plant resistance towards insects.
XX CC Specifically, the toxicity of the present sequence towards Diabrotica
XX CC virgifera virgifera was tested. The EC50 value (concentration at which
XX CC 50% feeding inhibition is observed) of the present protein was found to
XX CC be 7.12 microgram per millilitre, compared to 4.04 microgram per
XX CC millilitre for the wild type CryIIIA protein.
XX CC note: this sequence does not appear in the specification; it was created
XX CC using information provided.
XX CC
XX Sequence 644 AA:
XX
XX Query Match 84.3%; Score 543; DB 18; Length 644;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MNPNNSEHDTKTENNENPTNHYOYPLAETPNPTLEDLNTKEFLRMADNTEALDSS 60
XX DB 1 MNPNNSEHDTKTENNENPTNHYOYPLAETPNPTLEDLNTKEFLRMADNTEALDSS 60
XX QY 61 TTRDVIOKGISVVDLGIVGFPFGALVSFTYNTLTIIPSEDPKAKMEQVEALMDOK 120
XX DB 61 TTRDVIOKGISVVDLGIVGFPFGALVSFTYNTLTIIPSEDPKAKMEQVEALMDOK 120
XX QY 121 IADYAKNKALAELOGIÖNNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSQAESHFRRNS 180
XX DB 121 IADYAKNKALAELOGIÖNNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSQAESHFRRNS 180

```

```

DB 121 IADYAKNKALAELOGIÖNNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSQAESHFRRNS 180
QY 181 MPEFAISGEVLEFLTTYQAANTHLFLKDAQIYEENKYEKEDIAEYRKROLKLTQET 240
DB 181 MPEFAISGEVLEFLTTYQAANTHLFLKDAQIYEENKYEKEDIAEYRKROLKLTQET 240
QY 241 DHCVKMYNGLKLGSSYESVWNNRYRREMTLVLDLALFPLYDRLVPKYEKTEL 300
DB 241 DHCVKMYNGLKLGSSYESVWNNRYRREMTLVLDLALFPLYDRLVPKYEKTEL 300
QY 301 RDVLDPPIVGVNNLRGSGTTFSENIENYIRKPHLFDYLRHQFHTFRQPGYGNDSFNWMS 360
DB 301 RDVLDPPIVGVNNLRGSGTTFSENIENYIRKPHLFDYLRHQFHTFRQPGYGNDSFNWMS 360
QY 361 GNYVSTRPSIGSNDITTSFFYGNKSSEPVQNLFEFGEYVYRAVANTNLAVPSAVSGVT 420
DB 361 GNYVSTRPSIGSNDITTSFFYGNKSSEPVQNLFEFGEYVYRAVANTNLAVPSAVSGVT 420
QY 421 KYEFSQYNDQTEASTQYTDKSRNKGAVAMSDIDLPETTDDEPLEKGYSHOLNVMCFL 480
DB 421 KYEFSQYNDQTEASTQYTDKSRNKGAVAMSDIDLPETTDDEPLEKGYSHOLNVMCFL 480
QY 481 MOGSRTGIPVLNTHKSVDFENMIDSKKITQLELVKAYKLGASVAVGPRFTGGDIIOC 540
DB 481 MOGSRTGIPVLNTHKSVDFENMIDSKKITQLELVKAYKLGASVAVGPRFTGGDIIOC 540
QY 541 TENGSAATITVYPDVYSQKRYARIRHYASTQITTTSLDGAFFQYTFDXTINKGDTLT 600
DB 541 TENGSAATITVYPDVYSQKRYARIRHYASTQITTTSLDGAFFQYTFDXTINKGDTLT 600
QY 601 YNSFNLASFTPELGSNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFTPELGSNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
RESULT 36
AAM34830
ID AAM34830 standard; Protein: 644 AA.
XX
XX AC AAM34830;
XX DT 25-FEB-1998 (first entry)
XX DE Novel CryIIIA mutant protein G310A.
XX KM CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
XX KM increased toxicity; Coleopteran insect; Colorado potato beetle;
XX KM relative solvent accessibility; plant resistance;
XX KM Diabrotica virgifera virgifera.
XX OS Synthetic.
XX OS Bacillus thuringiensis.
XX FT Key Location/Qualifiers
XX FT Misc-difference 310 /label= G310A
XX FT /note= "wild type Gly replaced with Ala"
XX
XX PN US5659123-A.
XX PD 19-AUG-1997.
XX PE 26-AUG-1994; 94US-0295060.
XX PR 26-AUG-1994; 94US-0295060.
XX PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
XX PI Jansens S, Peferoen M, Van Rie J;
XX DR WPI: 1997-424316/39.
XX

```



```

OY 61 TTKDVIQGISVGGDLGAVGFPFGALVSEYTFNPLANTIMPSDDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQGISVGGDLGAVGFPFGALVSEYTFNPLANTIMPSDDPKAFMEQVEALMDOK 120
OY 121 IADYAKKAKALAELOGLONNVEDYVSALLSSQKNPVSSNPNHSGRIRELFSQASHFRNS 180
DB 121 IADYAKKAKALAELOGLONNVEDYVSALLSSQKNPVSSNPNHSGRIRELFSQASHFRNS 180
OY 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGYEKEDIAPFKRQKLTOEYT 240
DB 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGYEKEDIAPFKRQKLTOEYT 240
OY 241 DHCVMYVNGDLKLGSSYSESVNENRYRREMTLVLIDLALPLDYRLYPKEVTELT 300
DB 241 DHCVMYVNGDLKLGSSYSESVNENRYRREMTLVLIDLALPLDYRLYPKEVTELT 300
OY 301 RDVLTDPYGVNMLRGYGTTSNENYIRKPHLEDFYLRHIOFHTROPQGYGDSFNYS 360
DB 301 RDVLTDPYGVNMLRGYGTTSNENYIRKPHLEDFYLRHIOFHTROPQGYGDSFNYS 360
OY 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
OY 421 KVEFSQYNDQDEASTQYDYSKRNVAVSMDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
DB 421 KVEFSQYNDQDEASTQYDYSKRNVAVSMDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
OY 481 MGSRGITPVLWTWTHKSVDFENMIDSKKITQPLVKAKKLGSGASVAVAGPRTGGDIIOC 540
DB 481 MGSRGITPVLWTWTHKSVDFENMIDSKKITQPLVKAKKLGSGASVAVAGPRTGGDIIOC 540
OY 541 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 600
DB 541 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 600
OY 601 YNSENLASFSFPELGSNNLIQVGTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSENLASFSFPELGSNNLIQVGTGLSAGDKVYIDKIEFIPVN 644

RESULT 38
AAM34832
ID AAM34832 standard; Protein: 644 AA.
XX
AC AAM34832:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein L408A.
XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein:
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW relative solvent accessibility; plant resistance;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT MISC-difference 408 /label= "L408A
FT /note= "wild type Leu replaced with Ala"
XX
PN US5659123-A.
XX
PD 19-AUG-1997.
XX
PE 26-AUG-1994; 94US-0295060.
XX
PR 26-AUG-1994; 94US-0295060.
XX
PA (PLBZ ) PLANT GENETIC SYSTEMS NV.

```

```

XX Jansens S, Peferoen M, Van Rie J;
PI WPI: 1997-424316/39.
XX
DR Modified Bacillus thuringiensis CryIII proteins - with increased
XX toxicity against insect pests, particularly Coleopteran insects,
XX e.g. corn rootworm and Colorado potato beetle
XX
PS Example 1; Page -: 22pp; English.
XX
CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested. The EC50 value (concentration at which
CC 50% feeding inhibition is observed) of the present protein was found to
CC be 4.29 microgram per millilitre, compared to 3.08 microgram per
CC millilitre for the wild type CryIIIA protein.
CC note: this sequence does not appear in the specification: it was created
CC using information provided.
XX
SQ Sequence 644 AA:
XX
Query Match 84.3%; Score 543; DB 18; Length 644;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MNPNNRSEHDTIKITENNEVPJNHVOYPLAETPNPTLEDLNYKFLRMTADNNTALDSS 60
DB 1 MNPNNRSEHDTIKITENNEVPJNHVOYPLAETPNPTLEDLNYKFLRMTADNNTALDSS 60
OY 61 TTKDVIQGISVGGDLGAVGFPFGALVSEYTFNPLANTIMPSDDPKAFMEQVEALMDOK 120
DB 61 TTKDVIQGISVGGDLGAVGFPFGALVSEYTFNPLANTIMPSDDPKAFMEQVEALMDOK 120
OY 121 IADYAKKAKALAELOGLONNVEDYVSALLSSQKNPVSSNPNHSGRIRELFSQASHFRNS 180
DB 121 IADYAKKAKALAELOGLONNVEDYVSALLSSQKNPVSSNPNHSGRIRELFSQASHFRNS 180
OY 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGYEKEDIAPFKRQKLTOEYT 240
DB 181 MPFAISGEVLEFLTYQAANTHLEFLKDAQIYGEEMGYEKEDIAPFKRQKLTOEYT 240
OY 241 DHCVMYVNGDLKLGSSYSESVNENRYRREMTLVLIDLALPLDYRLYPKEVTELT 300
DB 241 DHCVMYVNGDLKLGSSYSESVNENRYRREMTLVLIDLALPLDYRLYPKEVTELT 300
OY 301 RDVLTDPYGVNMLRGYGTTSNENYIRKPHLEDFYLRHIOFHTROPQGYGDSFNYS 360
DB 301 RDVLTDPYGVNMLRGYGTTSNENYIRKPHLEDFYLRHIOFHTROPQGYGDSFNYS 360
OY 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVONLEFNGEKYRAVANNTLAWPSAVYSGVT 420
OY 421 KVEFSQYNDQDEASTQYDYSKRNVAVSMDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
DB 421 KVEFSQYNDQDEASTQYDYSKRNVAVSMDSIDQLPETTDEPLEKGYSHOLNYVMCFL 480
OY 481 MGSRGITPVLWTWTHKSVDFENMIDSKKITQPLVKAKKLGSGASVAVAGPRTGGDIIOC 540
DB 481 MGSRGITPVLWTWTHKSVDFENMIDSKKITQPLVKAKKLGSGASVAVAGPRTGGDIIOC 540
OY 541 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 600
DB 541 TENGSAATYVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNOYFDDTKINKGDTLT 600

```

DB 541 TENGSAATITVTPDVSYSQYRARIHYASTSQITFTLLSDGAFNQYFDKTIKNGDTLT 600
 QY 601 YNSFNLASFSPTPELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSPTPELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644

RESULT 39
 AAW34833
 ID AAW34833 standard; Protein: 644 AA.
 AC AAW34833;
 DT 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein P348A.
 XX
 XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH Key Location/Qualifiers
 FT Misc-difference 348 /label= P348A
 FT /note= "wild type Pro replaced with Ala"
 FT
 FT US5659123-A.
 PD 19-AUG-1997.
 XX
 XX 26-AUG-1994; 94US-0295060.
 PF
 PR 26-AUG-1994; 94US-0295060.
 XX
 XX (PLBZ) PLANT GENETIC SYSTEMS NV.
 PA
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI; 1997-424316/39.
 XX
 PT Modified Bacillus thuringiensis CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 PS
 PS Claim 18; Page -: 22pp; English.
 XX
 XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 12.47 microgram per millilitre, compared to 3.08 microgram per
 CC millilitre for the wild type CryIIIA protein. This mutant protein is
 CC recognised as a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification. It was created
 CC using information provided.
 XX
 XX Sequence 644 AA;
 SQ

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKTTENNEVPYTHVQYPLAETNPPLLEDLNTYKEFLRMADNNTTEALDSS 60
 DB 1 MNPNNSEHDTIKTTENNEVPYTHVQYPLAETNPPLLEDLNTYKEFLRMADNNTTEALDSS 60
 QY 61 TTKDVIOKGISVYGDLLGVGPPFGALVSFYTNPLNTIMPSDEPKAFMEOVEALMDOK 120
 DB 61 TTKDVIOKGISVYGDLLGVGPPFGALVSFYTNPLNTIMPSDEPKAFMEOVEALMDOK 120
 QY 121 IADYAKKALAELOGLONNEDYVSALSSQKMPVSSRNPHSGRIRELFSQASHFRNS 180
 DB 121 IADYAKKALAELOGLONNEDYVSALSSQKMPVSSRNPHSGRIRELFSQASHFRNS 180
 QY 181 MPSPAIISGEVLEFLTYQAANTHLFLKDAQIYGEEMYEKEDIAEFYKRLQKLTQEYT 240
 DB 181 MPSPAIISGEVLEFLTYQAANTHLFLKDAQIYGEEMYEKEDIAEFYKRLQKLTQEYT 240
 QY 241 DHCYKMYNNGLDKRGSSYSWVNFNRYREMTLVLDLALFPLVDVRLYPREVKTETL 300
 DB 241 DHCYKMYNNGLDKRGSSYSWVNFNRYREMTLVLDLALFPLVDVRLYPREVKTETL 300
 QY 301 RDVLTDPYGVNMLRGYGTFFSNIENTYIRKPHLEFDYLHRIQFHTRPQGYGNDSEFNYS 360
 DB 301 RDVLTDPYGVNMLRGYGTFFSNIENTYIRKPHLEFDYLHRIQFHTRPQGYGNDSEFNYS 360
 QY 361 GNYVSTRPSIGSNDIITSPYGNKSSSEPVONLEPNEGKRYRAVANNTNLAVPSAVYSQVT 420
 DB 361 GNYVSTRPSIGSNDIITSPYGNKSSSEPVONLEPNEGKRYRAVANNTNLAVPSAVYSQVT 420
 QY 421 KVERSOYNDQDDEASTQTYDSKRNVGAVSWDSIDOLPPEITDPLRKGYSHOANTYMCFL 480
 DB 421 KVERSOYNDQDDEASTQTYDSKRNVGAVSWDSIDOLPPEITDPLRKGYSHOANTYMCFL 480
 QY 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQLPLVAKYKLGASVAVAGPRTGDIIOC 540
 DB 481 MGSRGITPVLWTHKSVDFEPMIDSKKITQLPLVAKYKLGASVAVAGPRTGDIIOC 540
 QY 541 TENGSAATITVTPDVSYSQYRARIHYASTSQITFTLLSDGAFNQYFDKTIKNGDTLT 600
 DB 541 TENGSAATITVTPDVSYSQYRARIHYASTSQITFTLLSDGAFNQYFDKTIKNGDTLT 600
 QY 601 YNSFNLASFSPTPELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
 DB 601 YNSFNLASFSPTPELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644

RESULT 40
 AAW34834
 ID AAW34834 standard; Protein: 644 AA.
 AC AAW34834;
 DT 25-FEB-1998 (first entry)
 DE Novel CryIIIA mutant protein I376A.
 XX
 XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM Diabrotica virgifera virgifera.
 OS Synthetic.
 OS Bacillus thuringiensis.
 FH Key Location/Qualifiers
 FT Misc-difference 376 /label= I376A
 FT /note= "wild type Ile replaced with Ala"
 FT
 FT US5659123-A.
 PN

CC note: this sequence does not appear in the specification: it was created
 CC using information provided.

SO Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MNPNNRSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
DB 1 MNPNNRSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60
OY 61 TTKDVIQKGISVYVGDLLGVYGFPGALVSFTYNTLNTIMPSEDPWKAFFMEQVEALMDOK 120
DB 61 TTKDVIQKGISVYVGDLLGVYGFPGALVSFTYNTLNTIMPSEDPWKAFFMEQVEALMDOK 120
OY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNPVSSRRPHSOGRIREFLSQAESHFRNS 180
DB 121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNPVSSRRPHSOGRIREFLSQAESHFRNS 180
OY 181 MPSPAIISGEVLEFLTTTAAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240
DB 181 MPSPAIISGEVLEFLTTTAAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240
OY 241 DHCVKWYVNGLDLKGSSYESWVNNRRYRREMTLVLDLALFPLYDRLPKKVKTELT 300
DB 241 DHCVKWYVNGLDLKGSSYESWVNNRRYRREMTLVLDLALFPLYDRLPKKVKTELT 300
OY 301 RDVLTPPIVGVNNLKGYSYTTFSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360
DB 301 RDVLTPPIVGVNNLKGYSYTTFSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360
OY 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420
DB 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420
OY 421 KVESQYNDQDEASTQYTDKSRNRYGAVSMDSIDOLPEPTDEPLEKGYSHQNLVWCF 480
DB 421 KVESQYNDQDEASTQYTDKSRNRYGAVSMDSIDOLPEPTDEPLEKGYSHQNLVWCF 480
OY 481 MOGSRTPIVLTWTHKSVDFNMDSKRTIQLPLVKAVKLOSASVYAGPFTGDIIOC 540
DB 481 MOGSRTPIVLTWTHKSVDFNMDSKRTIQLPLVKAVKLOSASVYAGPFTGDIIOC 540
OY 541 TENGSAATIVYTPDYSYQKRYRARIHYASTQITFTLSLDGAPNOYFFDITINKGDTLT 600
DB 541 TENGSAATIVYTPDYSYQKRYRARIHYASTQITFTLSLDGAPNOYFFDITINKGDTLT 600
OY 601 YNSFNLAFFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLAFFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

```

RESULT 42

AAW34836 standard; Protein: 644 AA.

AC AAW34836;

DT 25-FEB-1998 (first entry)

DE Novel CryIIIA mutant protein I375A.

KX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;

KM Increased toxicity; Coleopteran insect; Colorado potato beetle;

KW relative solvent accessibility; plant resistance;

KX Diabrotica virgifera virgifera.

OS Synthetic.

XX Bacillus thuringiensis.

XX Key

Location/Qualifiers

FT Misc-difference 375
 FT /label= I375A
 FT /note="wild type Ile replaced with Ala"

XX US5659123-A.

XX 19-AUG-1997.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

XX (PLB2) PLANT GENETIC SYSTEMS NY.

XX Jansens S, Peferoen M, Van Rie J;

XX WPI; 1997-424316/39.

XX Modified Bacillus thuringiensis CryIII proteins - with increased

XX toxicity against insect pests, particularly Coleopteran insects,

XX e.g. corn rootworm and Colorado potato beetle

XX Example 1; Page -: 22pp; English.

XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning

XX mutagenesis of domain II of the CryIIIA protein of Bacillus

XX thuringiensis. All the positions changed to alanine in these proteins

XX are located in some of the solvent exposed loops and beta-strands

XX directed towards or located at the molecular apex. The substituted amino

XX acids have a relative solvent accessibility of at least 40%, or are a

XX maximum distance of 3 amino acids away from an amino acid having at least

XX 40% relative solvent accessibility. The novel CryIIIA proteins have an

XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

XX and can be used to combat, or improve plant resistance towards insects.

XX Specifically, the toxicity of the present sequence towards Diabrotica

XX virgifera virgifera was tested. The EC50 value (concentration at which

XX 50% feeding inhibition is observed) of the present protein was found to

XX be 1.65 microgram per millilitre, compared to 0.95 microgram per

XX millilitre for the wild type CryIIIA protein.

XX note: this sequence does not appear in the specification: it was created

XX using information provided.

XX Sequence 644 AA:

XX Query Match 84.3%; Score 543; DB 18; Length 644;

XX Best Local Similarity 99.8%; Pred. No. 0;

XX Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 MNPNNRSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60

XX 1 MNPNNRSEHDTIKTTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMTADNNTALDSS 60

XX 61 TTKDVIQKGISVYVGDLLGVYGFPGALVSFTYNTLNTIMPSEDPWKAFFMEQVEALMDOK 120

XX 61 TTKDVIQKGISVYVGDLLGVYGFPGALVSFTYNTLNTIMPSEDPWKAFFMEQVEALMDOK 120

XX 121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNPVSSRRPHSOGRIREFLSQAESHFRNS 180

XX 121 IADYAKNKALAELOGLQNNVEDYVSALSSWOKNPVSSRRPHSOGRIREFLSQAESHFRNS 180

XX 181 MPSPAIISGEVLEFLTTTAAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240

XX 181 MPSPAIISGEVLEFLTTTAAANTHLFLKDAQIYGEEMGEKEDIAPFYKROLKLTQEXT 240

XX 241 DHCVKWYVNGLDLKGSSYESWVNNRRYRREMTLVLDLALFPLYDRLPKKVKTELT 300

XX 241 DHCVKWYVNGLDLKGSSYESWVNNRRYRREMTLVLDLALFPLYDRLPKKVKTELT 300

XX 301 RDVLTPPIVGVNNLKGYSYTTFSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360

XX 301 RDVLTPPIVGVNNLKGYSYTTFSNIENYIRKPHLEDYLRHIOFHTRFOPGYGNDSPFNWS 360

XX 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420

XX 361 GNYVSTRPSIGSNDIITSPFYGNKSSEPVONLEFNGEKYRAVANTNLAVWPSAVYSGVT 420

```

Db 361 GNYSTRPSISGNDIITSPFYGNKSSSEPVQNLFEENGKRYRAVANTNLAVWPSAVSGVT 420
QY 421 KVEFSQYNDQTDASTQYDYSKRNVAWSMDISDLPETTDDEPLEKGYSHQNLVWCF 480
Db 421 KVEFSQYNDQTDASTQYDYSKRNVAWSMDISDLPETTDDEPLEKGYSHQNLVWCF 480
QY 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKYLOSASVYAGPRFTGGDIQC 540
Db 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKYLOSASVYAGPRFTGGDIQC 540
QY 541 TENGSAATITVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNQYFEDTKINKGDTLT 600
Db 541 TENGSAATITVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNQYFEDTKINKGDTLT 600
QY 601 YNSFNLASFTSPPELSCNNIQTGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLASFTSPPELSCNNIQTGVTGLSAGDKVYIDKIEFTIPVN 644

```

RESULT 43

AAW34837

ID AAW34837 standard; Protein: 644 AA.

AC AAW34837;

DT 25-FEB-1998 (first entry)

DE Novel CryIIIA mutant protein Y416A.

XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;

KW increased toxicity; Coleopteran insect; Colorado potato beetle;

KM relative solvent accessibility; plant resistance;

XX Diabrotica virgifera virgifera.

OS Synthetic.

XX Bacillus thuringiensis.

FH Key location/Qualifiers

FT Misc-difference 416

FT /label- Y416A

FT /note- "wild type Tyr replaced with Ala"

XX US5659123-A.

XX 19-AUG-1997.

XX 26-AUG-1994; 94US-0295060.

XX 26-AUG-1994; 94US-0295060.

XX (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Janssens S, Peferoen M, Van Rie J;

XX WPI: 1997-424316/39.

XX Claim 9; Page -: 22pp; English.

XX Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning

XX mutagenesis of domain II of the CryIIIA protein of Bacillus

XX thuringiensis. All the positions changed to alanine in these proteins

XX are located in some of the solvent exposed loops and beta-strands

XX directed towards or located at the molecular apex. The substituted amino

XX acids have a relative solvent accessibility of at least 40%, or are a

XX maximum distance of 3 amino acids away from an amino acid having at least

XX 40% relative solvent accessibility. The novel CryIIIA proteins have an

XX increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,

XX and can be used to combat, or improve plant resistance towards insects.

Specifically, the toxicity of the present sequence towards Diabrotica virgifera virgifera was tested. The EC50 value (concentration at which 50% feeding inhibition is observed) of the present protein was found to be >256 microgram per millilitre, compared to 3.82 microgram per millilitre for the wild type CryIIIA protein. This mutant protein is recognised as a "down mutant" for Diabrotica virgifera virgifera. The toxicity of the mutant protein for this Diabrotica pest was significantly below the toxicity of the native CryIIIA protein. CC note: this sequence does not appear in the specification; it was created using information provided.

SQ Sequence 644 AA:

Query Match 84.3%; Score 543; DB 18; Length 644;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MNPNNRSEHDTIKTTENNEVPYTHVOYPLAETPNPTLEDLNTYKEFLMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTTENNEVPYTHVOYPLAETPNPTLEDLNTYKEFLMTADNNTALDSS 60
QY 61 TTKDVIQKISVYGDLLGVVGFPPGALVSFTYNTPLNTIPSDPPKATMEQVEALMDOK 120
Db 61 TTKDVIQKISVYGDLLGVVGFPPGALVSFTYNTPLNTIPSDPPKATMEQVEALMDOK 120
QY 121 IADYAKKALAELOGLQNNVEDYVLSALSMQKPNVSSRNPHSGRIRLEFSQASHFRNS 180
Db 121 IADYAKKALAELOGLQNNVEDYVLSALSMQKPNVSSRNPHSGRIRLEFSQASHFRNS 180
QY 181 MPSPASIGYEVLETTYAQAANTHFLKDAQITGEGMEYKEDIAEFYKROKLTQEXT 240
Db 181 MPSPASIGYEVLETTYAQAANTHFLKDAQITGEGMEYKEDIAEFYKROKLTQEXT 240
QY 241 DHCYKMYNGLDKLRGSSYSWVNFNRYRREMLTYVDLALPLVDVRLYPREVTELT 300
Db 241 DHCYKMYNGLDKLRGSSYSWVNFNRYRREMLTYVDLALPLVDVRLYPREVTELT 300
QY 301 RDVLTDPYGVNNLRGTYGTFNSIENTYIRKPHLEFDYLRHQFTFRPOPQYGGNDSFNYS 360
Db 301 RDVLTDPYGVNNLRGTYGTFNSIENTYIRKPHLEFDYLRHQFTFRPOPQYGGNDSFNYS 360
QY 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVQNLFEENGKRYRAVANTNLAVWPSAVSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPFYGNKSSSEPVQNLFEENGKRYRAVANTNLAVWPSAVSGVT 420
QY 421 KVEFSQYNDQTDASTQYDYSKRNVAWSMDISDLPETTDDEPLEKGYSHQNLVWCF 480
Db 421 KVEFSQYNDQTDASTQYDYSKRNVAWSMDISDLPETTDDEPLEKGYSHQNLVWCF 480
QY 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKYLOSASVYAGPRFTGGDIQC 540
Db 481 MGSRGITPVLWTHTKSVDFEENMDSKKTQLPLVKAKYLOSASVYAGPRFTGGDIQC 540
QY 541 TENGSAATITVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNQYFEDTKINKGDTLT 600
Db 541 TENGSAATITVTPDVYSQKRYRARIHYASTQITFTLSLDGAPFNQYFEDTKINKGDTLT 600
QY 601 YNSFNLASFTSPPELSCNNIQTGVTGLSAGDKVYIDKIEFTIPVN 644
Db 601 YNSFNLASFTSPPELSCNNIQTGVTGLSAGDKVYIDKIEFTIPVN 644

```

RESULT 44

AAW34838

ID AAW34838 standard; Protein: 644 AA.

AC AAW34838;

DT 25-FEB-1998 (first entry)

DE Novel CryIIIA mutant protein Y327A.

XX CryIIIA gene; corn rootworm toxicity; CryIIIA protein;

KM Increased toxicity: Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility: plant resistance;
 KM *Diabrotica virgifera virgifera*.
 XX
 OS Synthetic.
 OS *Bacillus thuringiensis*.
 FH Key Location/Qualifiers
 FT Misc-difference 327 /label= Y327A
 FT /note= "wild type Trp replaced with Ala"
 PN US5659123-A.
 PD 19-AUG-1997.
 XX
 XX 26-AUG-1994: 94US-0295060.
 XX
 XX 26-AUG-1994: 94US-0295060.
 XX
 XX (PLBZ) PLANT GENETIC SYSTEMS NV.
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI: 1997-424316/39.
 XX
 XX Modified *Bacillus thuringiensis* CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 XX Example 1; Page -: 22pp; English.
 XX
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of *Bacillus*
 CC *thuringiensis*. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards *Diabrotica*
 CC *virgifera virgifera* was tested. The EC50 value (concentration at which
 CC 50% feeding inhibition is observed) of the present protein was found to
 CC be 2.40 microgram per millilitre, compared to 3.82 microgram per
 CC millilitre for the wild type CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 CC
 CC Sequence 644 AA:
 SQ
 Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNPNNRSEHDITKTENNEVPNHNQVPLAETPNPTLEDLNKKEPLRTADNNTFALDSS 60
 DB 1 MNPNNRSEHDITKTENNEVPNHNQVPLAETPNPTLEDLNKKEPLRTADNNTFALDSS 60
 QY 61 TTKDVIYQKGISVAGDGLGVGFPFGALVSFTYTNFLNTIMPSEDPWKAFMQVEALMDOK 120
 DB 61 TTKDVIYQKGISVAGDGLGVGFPFGALVSFTYTNFLNTIMPSEDPWKAFMQVEALMDOK 120
 QY 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPYSNRNPHSQGIRIRLFQASHEHFNNS 180
 DB 121 IADYAKNKALAELOGLONNVEDYVSALSSWQKNPYSNRNPHSQGIRIRLFQASHEHFNNS 180
 QY 181 MPSFAISGVEVFLFTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKQKOLKTOEY 240
 DB 181 MPSFAISGVEVFLFTTYQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKQKOLKTOEY 240
 QY 241 DHCWKWYVGLDKLRGSSYESWVNNRYRREMTLTVDLIALFPLVDVRLYKPEVKTELT 300

DB 241 DHCWKWYVGLDKLRGSSYESWVNNRYRREMTLTVDLIALFPLVDVRLYKPEVKTELT 300
 QY 301 RDVLTDPVGVNNLRGCTFTSENIENTIRKPHLFDYLRHQFHTRPGYTGDSFNWYS 360
 DB 301 RDVLTDPVGVNNLRGCTFTSENIENTIRKPHLFDYLRHQFHTRPGYTGDSFNWYS 360
 QY 361 GNYVSTRSISGNDIITSPFGNKSSEPVONLENGEKYRAVANNTLAWPSPAVISGVT 420
 DB 361 GNYVSTRSISGNDIITSPFGNKSSEPVONLENGEKYRAVANNTLAWPSPAVISGVT 420
 QY 421 KVEFSQYNDQDEASTQYDYSKRNWGAVSWSIDQLPPTTDEPLEKGYSHQUNYWCFL 480
 DB 421 KVEFSQYNDQDEASTQYDYSKRNWGAVSWSIDQLPPTTDEPLEKGYSHQUNYWCFL 480
 QY 481 MGSRGITIPVLTWTHKSVDFNMIDSKKITQPLVKAYKLGASVAVAGPRTGGDIIOC 540
 DB 481 MGSRGITIPVLTWTHKSVDFNMIDSKKITQPLVKAYKLGASVAVAGPRTGGDIIOC 540
 QY 541 TENGSAATIVYTPDVSYSSQYRARIRHASTQITFTLSLDCAPFNQYFPDKTINKGDTLT 600
 DB 541 TENGSAATIVYTPDVSYSSQYRARIRHASTQITFTLSLDCAPFNQYFPDKTINKGDTLT 600
 QY 601 YNSFNLASFTPELSCGNLQIGVTGLSAGDKYIDKIEFIPVN 644
 DB 601 YNSFNLASFTPELSCGNLQIGVTGLSAGDKYIDKIEFIPVN 644
 RESULT 45
 AAW34839
 ID AAW34839 standard; Protein; 644 AA.
 XX
 AC AAW34839;
 XX
 DT 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein F346A.
 XX
 KM CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
 KM increased toxicity; Coleopteran insect; Colorado potato beetle;
 KM relative solvent accessibility; plant resistance;
 KM *Diabrotica virgifera virgifera*.
 XX
 OS Synthetic.
 OS *Bacillus thuringiensis*.
 FH Key Location/Qualifiers
 FT Misc-difference 346 /label= F346A
 FT /note= "wild type Phe replaced with Ala"
 PN US5659123-A.
 PD 19-AUG-1997.
 XX
 XX 26-AUG-1994: 94US-0295060.
 XX
 XX 26-AUG-1994: 94US-0295060.
 XX
 XX (PLBZ) PLANT GENETIC SYSTEMS NV.
 PI Jansens S, Peferoen M, Van Rie J;
 DR WPI: 1997-424316/39.
 XX
 XX Modified *Bacillus thuringiensis* CryIII proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle
 XX
 XX Claim 9; Page -: 22pp; English.
 CC Novel CryIIIA proteins AAW34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIIA protein of *Bacillus*

CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested, and the present mutant protein was
 CC found to be a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

CC Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 OY 61 TTKDVIQKIGSVGGDLGVGFPFGALVSFTYNTFNTIMPSDEDPKAFMEQVEALMDQK 120
 DB 61 TTKDVIQKIGSVGGDLGVGFPFGALVSFTYNTFNTIMPSDEDPKAFMEQVEALMDQK 120
 OY 121 IADYAKNKALALQGLQNNVEDYVSSALSSWQKNPVSRRNPSSQGRIRLEFSQAESHFRRNS 180
 DB 121 IADYAKNKALALQGLQNNVEDYVSSALSSWQKNPVSRRNPSSQGRIRLEFSQAESHFRRNS 180
 OY 121 IADYAKNKALALQGLQNNVEDYVSSALSSWQKNPVSRRNPSSQGRIRLEFSQAESHFRRNS 180
 DB 121 IADYAKNKALALQGLQNNVEDYVSSALSSWQKNPVSRRNPSSQGRIRLEFSQAESHFRRNS 180
 OY 181 MPEFASIGYEVLEFITYQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
 DB 181 MPEFASIGYEVLEFITYQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEXT 240
 OY 241 DHCWKYRNVGDLKRGSSYEVNVRNRIRREMTLVLDLALFPLVDRLXPKKVEKTELT 300
 DB 241 DHCWKYRNVGDLKRGSSYEVNVRNRIRREMTLVLDLALFPLVDRLXPKKVEKTELT 300
 OY 241 DHCWKYRNVGDLKRGSSYEVNVRNRIRREMTLVLDLALFPLVDRLXPKKVEKTELT 300
 DB 241 DHCWKYRNVGDLKRGSSYEVNVRNRIRREMTLVLDLALFPLVDRLXPKKVEKTELT 300
 OY 301 RDVLTPPIYGVNNLRGCTGTFSENIENYIRKPLFDYLRHIOPTHFQGGYGNDSFNYS 360
 DB 301 RDVLTPPIYGVNNLRGCTGTFSENIENYIRKPLFDYLRHIOPTHFQGGYGNDSFNYS 360
 OY 301 RDVLTPPIYGVNNLRGCTGTFSENIENYIRKPLFDYLRHIOPTHFQGGYGNDSFNYS 360
 DB 301 RDVLTPPIYGVNNLRGCTGTFSENIENYIRKPLFDYLRHIOPTHFQGGYGNDSFNYS 360
 OY 361 GNVYSTRPSIGSNDITSPFYGNKSESPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 420
 DB 361 GNVYSTRPSIGSNDITSPFYGNKSESPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 420
 OY 421 KVEFSQYNDQTDASTQYTDSCRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLVWQEL 480
 DB 421 KVEFSQYNDQTDASTQYTDSCRNVGAVSWDSIDQLPPTTDEPLEKGYSHQNLVWQEL 480
 OY 481 MGSRGITPVLWTHTKSVGFNNIDSKKITQLPLVYKAYLQSGASVAVAGPRTGGDIQOC 540
 DB 481 MGSRGITPVLWTHTKSVGFNNIDSKKITQLPLVYKAYLQSGASVAVAGPRTGGDIQOC 540
 OY 541 TENGSAATIVTPDVVSQKYYRARIYASTQITFTLSLDGAPFNQYVYDKTINKGDLIT 600
 DB 541 TENGSAATIVTPDVVSQKYYRARIYASTQITFTLSLDGAPFNQYVYDKTINKGDLIT 600
 OY 601 YNSGNLASFTPELGGNNLQIGVGTLSAGDKYIDKIEFIPVN 644
 DB 601 YNSGNLASFTPELGGNNLQIGVGTLSAGDKYIDKIEFIPVN 644

RESULT 46
 AAM34840
 ID AAM34840 standard; Protein: 644 AA.
 AC AAM34840:
 XX
 XX

DE 25-FEB-1998 (first entry)
 XX
 DE Novel CryIIIA mutant protein Q347A.
 XX
 KW CryIIIA gene; corn rootworm toxicity; CryIIIA protein;
 KW increased toxicity; Coleopteran insect; Colorado potato beetle;
 KW relative solvent accessibility; plant resistance;
 KW Diabrotica virgifera virgifera.
 XX
 OS Synthetic.
 OS Bacillus thuringiensis.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 347 /label= Q347A
 FT /note="wild type Gln replaced with Ala"

PN US5659123-A.
 XX
 PD 19-AUG-1997.
 XX
 PF 26-AUG-1994; 94US-0295060.
 XX
 PR 26-AUG-1994; 94US-0295060.
 XX
 PA (PLBZ) PLANT GENETIC SYSTEMS NV.

XX Jansens S, Peferoen M, Van Rie J;
 XX WPI; 1997-424316/39.

PT Modified Bacillus thuringiensis CryIIA proteins - with increased
 PT toxicity against insect pests, particularly Coleopteran insects,
 PT e.g. corn rootworm and Colorado potato beetle

XX Claim 9; Page -: 22pp; English.

XX Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
 CC mutagenesis of domain II of the CryIIA protein of Bacillus
 CC thuringiensis. All the positions changed to alanine in these proteins
 CC are located in some of the solvent exposed loops and beta-strands
 CC directed towards or located at the molecular apex. The substituted amino
 CC acids have a relative solvent accessibility of at least 40%, or are a
 CC maximum distance of 3 amino acids away from an amino acid having at least
 CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
 CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
 CC and can be used to combat, or improve plant resistance towards insects.
 CC Specifically, the toxicity of the present sequence towards Diabrotica
 CC virgifera virgifera was tested, and the present mutant protein was
 CC found to be a "down mutant" for Diabrotica virgifera virgifera. The
 CC toxicity of the mutant protein for this Diabrotica pest was
 CC significantly below the toxicity of the native CryIIIA protein.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 644 AA;

Query Match 84.3%; Score 543; DB 18; Length 644;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 DB 1 MNPNNRSEHDTIKTTENNEVPYPLAETPNPTLEDLNTKEFLRMADNNTALDSS 60
 OY 61 TTKDVIQKIGSVGGDLGVGFPFGALVSFTYNTFNTIMPSDEDPKAFMEQVEALMDQK 120
 DB 61 TTKDVIQKIGSVGGDLGVGFPFGALVSFTYNTFNTIMPSDEDPKAFMEQVEALMDQK 120
 OY 121 IADYAKNKALALQGLQNNVEDYVSSALSSWQKNPVSRRNPSSQGRIRLEFSQAESHFRRNS 180
 DB 121 IADYAKNKALALQGLQNNVEDYVSSALSSWQKNPVSRRNPSSQGRIRLEFSQAESHFRRNS 180


```

OY 181 MSFSAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQET 240
    |||||||
Db 181 MSFSAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQET 240
OY 241 DHCWKYNNVGLDKLRGSSYESWVNNRYRREMTLVLDLIAFLPLYDRLPKREKTEL 300
    |||||||
Db 241 DHCWKYNNVGLDKLRGSSYESWVNNRYRREMTLVLDLIAFLPLYDRLPKREKTEL 300
OY 301 ROLVLDPIYGVNNLRGYGTTFSENIENYIRKPHLDYLRHQFHRFOPGTYGNDSEFN 360
    |||||||
Db 301 ROLVLDPIYGVNNLRGYGTTFSENIENYIRKPHLDYLRHQFHRFOPGTYGNDSEFN 360
OY 361 GNVYSTRPISGNDIITSPFYGNKSSPEVQNLFEENGEXYRAVANTNLAVWPSAVYSG 420
    |||||||
Db 361 GNVYSTRPISGNDIITSPFYGNKSSPEVQNLFEENGEXYRAVANTNLAVWPSAVYSG 420
OY 421 KVEFSQYNDQDEASTQTYDSKRNKAVGWSIDQLPEPTDEPLEKGYSHQNLVWVCF 480
    |||||||
Db 421 KVEFSQYNDQDEASTQTYDSKRNKAVGWSIDQLPEPTDEPLEKGYSHQNLVWVCF 480
OY 481 MGSRGITPVLWTWTKSVDFNMIDSKITQLPLVKAYKLGSGASVAVAGPFTGGDIQC 540
    |||||||
Db 481 MGSRGITPVLWTWTKSVDFNMIDSKITQLPLVKAYKLGSGASVAVAGPFTGGDIQC 540
OY 541 TENGAATITVTPDVYSQKTRARIHYASTQITFTLLSDGAPFNOYFPDKTINKGDTLT 600
    |||||||
Db 541 TENGAATITVTPDVYSQKTRARIHYASTQITFTLLSDGAPFNOYFPDKTINKGDTLT 600
OY 601 YNSFNLASFTPELSCGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
    |||||||
Db 601 YNSFNLASFTPELSCGNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 47
AAM34841
ID AAM34841 standard; Protein; 644 AA.
XX
AC AAM34841:
XX
DT 25-FEB-1998 (first entry)
XX
DE Novel CryIIIA mutant protein S442A.
XX
KW CryIIIA gene: corn rootworm toxicity; CryIIIA protein;
KW increased toxicity; Coleopteran insect; Colorado potato beetle;
KW Diabrotica virgifera virgifera.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT MISC-difference 442 /label= "S442A"
FT /note= "Wild type Ser replaced with Ala"
XX
PD US5659123-A.
XX
PD 19-AUG-1997.
XX
PF 26-AUG-1994: 94US-0295060.
XX
PR 26-AUG-1994: 94US-0295060.
XX
PA (PLB2 ) PLANT GENETIC SYSTEMS NV.
PI Jansens S, Peferoen M, Van Rie J;
DR WPI; 1997-424316/39.
XX
PT Modified Bacillus thuringiensis CryIII proteins - with increased
PT toxicity against insect pests, particularly Coleopteran insects,
e.g. corn rootworm and Colorado potato beetle

```

```

XX
PS Claim 9; Page -: 22pp; English.
XX
CC Novel CryIIIA proteins AAM34811-41 were produced by alanine scanning
CC mutagenesis of domain II of the CryIIIA protein of Bacillus
CC thuringiensis. All the positions changed to alanine in these proteins
CC are located in some of the solvent exposed loops and beta-strands
CC directed towards or located at the molecular apex. The substituted amino
CC acids have a relative solvent accessibility of at least 40%, or are a
CC maximum distance of 3 amino acids away from an amino acid having at least
CC 40% relative solvent accessibility. The novel CryIIIA proteins have an
CC increased toxicity to Coleopteran insects, e.g. Colorado potato beetle,
CC and can be used to combat, or improve plant resistance towards insects.
CC Specifically, the toxicity of the present sequence towards Diabrotica
CC virgifera virgifera was tested, and the present mutant protein was
CC found to be a "down mutant" for Diabrotica virgifera virgifera. The
CC toxicity of the mutant protein for this Diabrotica pest was
CC significantly below the toxicity of the native CryIIIA protein.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 644 AA;
OY 1 MNPNNRSEHDTIKTENNVEPTNHOYPLAETNPPTLEDLNKEFLRMTADNNTALDSS 60
Db 1 MNPNNRSEHDTIKTENNVEPTNHOYPLAETNPPTLEDLNKEFLRMTADNNTALDSS 60
OY 61 TTKDVIQKGISVVGDLGCVGFPEGGALVSFTNFNTNTIPSEDPKAKMEQVEALMDQK 120
Db 61 TTKDVIQKGISVVGDLGCVGFPEGGALVSFTNFNTNTIPSEDPKAKMEQVEALMDQK 120
OY 121 IADYAKKALAEIQLGQNNVEDYVSALSSWQKVPVSRPHSGRRLRELFSSQAEHSFNS 180
Db 121 IADYAKKALAEIQLGQNNVEDYVSALSSWQKVPVSRPHSGRRLRELFSSQAEHSFNS 180
OY 181 MFSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQET 240
Db 181 MFSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQET 240
OY 241 DHCWKYNNVGLDKLRGSSYESWVNNRYRREMTLVLDLIAFLPLYDRLPKREKTEL 300
Db 241 DHCWKYNNVGLDKLRGSSYESWVNNRYRREMTLVLDLIAFLPLYDRLPKREKTEL 300
OY 301 ROLVLDPIYGVNNLRGYGTTFSENIENYIRKPHLDYLRHQFHRFOPGTYGNDSEFN 360
Db 301 ROLVLDPIYGVNNLRGYGTTFSENIENYIRKPHLDYLRHQFHRFOPGTYGNDSEFN 360
OY 361 GNVYSTRPISGNDIITSPFYGNKSSPEVQNLFEENGEXYRAVANTNLAVWPSAVYSG 420
Db 361 GNVYSTRPISGNDIITSPFYGNKSSPEVQNLFEENGEXYRAVANTNLAVWPSAVYSG 420
OY 421 KVEFSQYNDQDEASTQTYDSKRNKAVGWSIDQLPEPTDEPLEKGYSHQNLVWVCF 480
Db 421 KVEFSQYNDQDEASTQTYDSKRNKAVGWSIDQLPEPTDEPLEKGYSHQNLVWVCF 480
OY 481 MGSRGITPVLWTWTKSVDFNMIDSKITQLPLVKAYKLGSGASVAVAGPFTGGDIQC 540
Db 481 MGSRGITPVLWTWTKSVDFNMIDSKITQLPLVKAYKLGSGASVAVAGPFTGGDIQC 540
OY 541 TENGAATITVTPDVYSQKTRARIHYASTQITFTLLSDGAPFNOYFPDKTINKGDTLT 600
Db 541 TENGAATITVTPDVYSQKTRARIHYASTQITFTLLSDGAPFNOYFPDKTINKGDTLT 600
OY 601 YNSFNLASFTPELSCGNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 601 YNSFNLASFTPELSCGNLQIGVTGLSAGDKVYIDKIEFIPVN 644

```

Search completed: January 10, 2003, 14:28:03

Fri Jan 10 14:49:33 2003

us-09-943-692-2.olig.rag

Page 37

Job time : 45 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:08:49 : Search time 16 Seconds

(without alignments)
1184.273 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644

Sequence: 1 MNPNRSEHDITKTENNEV.....TGLSAGDKYIDKIEFIPVN 644

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	644	100.0	644	1 US-07-828-788A-4	Sequence 4, Appl 1
2	644	100.0	644	1 US-08-072-281-2	Sequence 2, Appl 1
3	644	100.0	644	1 US-08-295-060-2	Sequence 2, Appl 1
4	644	100.0	644	1 US-08-759-446-2	Sequence 2, Appl 1
5	644	100.0	644	4 US-09-027-998A-2	Sequence 2, Appl 1
6	644	100.0	644	5 PCT-US92-11337-4	Sequence 4, Appl 1
7	644	100.0	652	3 US-08-996-441B-113	Sequence 113, App
8	644	100.0	652	3 US-08-993-722A-113	Sequence 113, App
9	644	100.0	652	3 US-08-993-170A-113	Sequence 113, App
10	644	100.0	652	3 US-08-993-775B-113	Sequence 113, App
11	597	92.7	597	3 US-08-704-966-2	Sequence 2, Appl 1
12	597	92.7	597	3 US-08-705-438-2	Sequence 2, Appl 1
13	595	92.4	610	3 US-08-704-966-4	Sequence 4, Appl 1
14	595	92.4	610	3 US-08-705-438-4	Sequence 4, Appl 1
15	344	53.4	645	1 US-08-295-060-4	Sequence 4, Appl 1
16	28	4.3	651	3 US-08-996-441B-56	Sequence 56, Appl 1
17	28	4.3	651	3 US-08-993-722A-56	Sequence 56, Appl 1
18	28	4.3	651	3 US-08-993-170A-56	Sequence 56, Appl 1
19	28	4.3	651	3 US-08-993-775B-56	Sequence 56, Appl 1
20	28	4.3	652	3 US-08-996-441B-46	Sequence 46, Appl 1
21	28	4.3	652	3 US-08-996-441B-50	Sequence 46, Appl 1
22	28	4.3	652	3 US-08-993-722A-46	Sequence 46, Appl 1
23	28	4.3	652	3 US-08-993-722A-50	Sequence 46, Appl 1
24	28	4.3	652	3 US-08-993-170A-46	Sequence 46, Appl 1
25	28	4.3	652	3 US-08-993-170A-50	Sequence 46, Appl 1
26	28	4.3	652	3 US-08-993-775B-46	Sequence 46, Appl 1
27	28	4.3	652	3 US-08-993-775B-50	Sequence 50, Appl 1

28	24	3.7	652	3	US-08-996-441B-44	Sequence 44, Appl 1
29	24	3.7	652	3	US-08-996-441B-60	Sequence 60, Appl 1
30	24	3.7	652	3	US-08-996-441B-62	Sequence 62, Appl 1
31	24	3.7	652	3	US-08-996-441B-66	Sequence 66, Appl 1
32	24	3.7	652	3	US-08-996-441B-108	Sequence 108, Appl 1
33	24	3.7	652	3	US-08-993-722A-108	Sequence 108, Appl 1
34	24	3.7	652	3	US-08-993-722A-60	Sequence 60, Appl 1
35	24	3.7	652	3	US-08-993-722A-62	Sequence 62, Appl 1
36	24	3.7	652	3	US-08-993-722A-66	Sequence 66, Appl 1
37	24	3.7	652	3	US-08-993-722A-108	Sequence 108, Appl 1
38	24	3.7	652	3	US-08-993-170A-44	Sequence 44, Appl 1
39	24	3.7	652	3	US-08-993-170A-60	Sequence 60, Appl 1
40	24	3.7	652	3	US-08-993-170A-62	Sequence 62, Appl 1
41	24	3.7	652	3	US-08-993-170A-66	Sequence 66, Appl 1
42	24	3.7	652	3	US-08-993-170A-108	Sequence 108, Appl 1
43	24	3.7	652	3	US-08-993-775B-44	Sequence 44, Appl 1
44	24	3.7	652	3	US-08-993-775B-60	Sequence 60, Appl 1
45	24	3.7	652	3	US-08-993-775B-62	Sequence 62, Appl 1

ALIGNMENTS

RESULT 1
US-07-828-788A-4
Sequence 4, Application US/07828788A
Patent No. 5273746
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIMANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
AMTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGERIENSIS
INDIVIDUAL ISOLATE: PS40D1
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF FRANK GAERTNER
CLONE: 40D1
US-07-828-788A-4

Query Match 100.0%; Score 644; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNPNNRSEHDITKTENNENVPNTNVOYPLAETPNPTLEDLNYKEFLKRLTADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNTNVOYPLAETPNPTLEDLNYKEFLKRLTADNNTALDSS 60
OY 61 TTKDVIOKGISVVDLGVGFPGGALVSFYTNFLNTIMPSEDPWKAEMOYVALMDOK 120
DB 61 TTKDVIOKGISVVDLGVGFPGGALVSFYTNFLNTIMPSEDPWKAEMOYVALMDOK 120
OY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
OY 181 MPSPAIISGYEVLFTTYAOANHTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
DB 181 MPSPAIISGYEVLFTTYAOANHTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
OY 241 DHCWKYVNWGLDKLRGSSYESWVNFNRYRREMTLVLDLALPPLVDVRLYPKEVTELT 300
DB 241 DHCWKYVNWGLDKLRGSSYESWVNFNRYRREMTLVLDLALPPLVDVRLYPKEVTELT 300
OY 301 RDVLTDPYVGNLRLGIGTFESNIENYIRKPHLEFDYLRHQFHTRFQPGYGGNDSFNWMS 360
DB 301 RDVLTDPYVGNLRLGIGTFESNIENYIRKPHLEFDYLRHQFHTRFQPGYGGNDSFNWMS 360
OY 361 GNYVSTRPSISGNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVYSGVT 420
DB 361 GNYVSTRPSISGNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVYSGVT 420
OY 421 KVEFSQYNDQTDASQYDYSKRNKAVSWDSIDQLPPTTDEPLEKGYSHOQNTYMCFL 480
DB 421 KVEFSQYNDQTDASQYDYSKRNKAVSWDSIDQLPPTTDEPLEKGYSHOQNTYMCFL 480
OY 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVAKYKLGASAVYAGPRTGGDIIOC 540
DB 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVAKYKLGASAVYAGPRTGGDIIOC 540
OY 541 TENGSAATIVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYDXTINKGDTLT 600
DB 541 TENGSAATIVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYDXTINKGDTLT 600
OY 601 YNSFNILASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIIPVN 644
DB 601 YNSFNILASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIIPVN 644

```

RESULT 2

US-08-072-281-2
 : Sequence 2, Application US/08072281
 : Patent No. 5495071
 : GENERAL INFORMATION:
 : APPLICANT: Fischhoff, David A.
 : APPLICANT: Fuchs, Roy L.
 : APPLICANT: Lawrik, Paul B.
 : APPLICANT: McPherson, Sylvia A.
 : APPLICANT: Perlick, Frederick J.
 : TITLE OF INVENTION: Insect Resistant Plants
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lawrence M. Lavin, Jr., Monsanto Co., BBAF
 : STREET: 700 Chesterfield Parkway No. 5495071th
 : CITY: St. Louis
 : STATE: Missouri
 : COUNTRY: United States of America
 : ZIP: 63198
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/072.281
 : FILING DATE: 19930604
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/523284
 : FILING DATE: 14-MAY-1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lavin Jr., Lawrence M.
 : REGISTRATION NUMBER: 30,768
 : REFERENCE/DOCKET NUMBER: 38-21(10629)A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (314) 537-7286
 : TELEFAX: (314) 537-6047
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 644 amino acids
 : TYPE: AMINO ACID
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-072-281-2

Query Match 100.0%; Score 644; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MNPNNRSEHDITKTENNENVPNTNVOYPLAETPNPTLEDLNYKEFLKRLTADNNTALDSS 60
DB 1 MNPNNRSEHDITKTENNENVPNTNVOYPLAETPNPTLEDLNYKEFLKRLTADNNTALDSS 60
OY 61 TTKDVIOKGISVVDLGVGFPGGALVSFYTNFLNTIMPSEDPWKAEMOYVALMDOK 120
DB 61 TTKDVIOKGISVVDLGVGFPGGALVSFYTNFLNTIMPSEDPWKAEMOYVALMDOK 120
OY 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
DB 121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGRIRLEFSQAESHRNS 180
OY 181 MPSPAIISGYEVLFTTYAOANHTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
DB 181 MPSPAIISGYEVLFTTYAOANHTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYT 240
OY 241 DHCWKYVNWGLDKLRGSSYESWVNFNRYRREMTLVLDLALPPLVDVRLYPKEVTELT 300
DB 241 DHCWKYVNWGLDKLRGSSYESWVNFNRYRREMTLVLDLALPPLVDVRLYPKEVTELT 300
OY 301 RDVLTDPYVGNLRLGIGTFESNIENYIRKPHLEFDYLRHQFHTRFQPGYGGNDSFNWMS 360
DB 301 RDVLTDPYVGNLRLGIGTFESNIENYIRKPHLEFDYLRHQFHTRFQPGYGGNDSFNWMS 360
OY 361 GNYVSTRPSISGNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVYSGVT 420
DB 361 GNYVSTRPSISGNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPSPAVYSGVT 420
OY 421 KVEFSQYNDQTDASQYDYSKRNKAVSWDSIDQLPPTTDEPLEKGYSHOQNTYMCFL 480
DB 421 KVEFSQYNDQTDASQYDYSKRNKAVSWDSIDQLPPTTDEPLEKGYSHOQNTYMCFL 480
OY 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVAKYKLGASAVYAGPRTGGDIIOC 540
DB 481 MOGSRGTIPVLTWTHKSVDFNMIDSKKITQPLVAKYKLGASAVYAGPRTGGDIIOC 540
OY 541 TENGSAATIVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYDXTINKGDTLT 600
DB 541 TENGSAATIVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYDXTINKGDTLT 600
OY 601 YNSFNILASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIIPVN 644
DB 601 YNSFNILASFSTPELSGNNLQIGVTGLSAGDKYIDKIEFIIPVN 644

```

RESULT 3

```

US-08-295-060-2
: Sequence 2, Application US/08295060
: Patent No. 5659123
:
GENERAL INFORMATION:
APPLICANT: VAN RIE, Jeroen
APPLICANT: JANSSEN, Stefan
APPLICANT: PEREREN, Marink
TITLE OF INVENTION: NEW DIABROTICA TOXINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,060
FILING DATE: 26-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Heury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-295-060-2

```

```

Db 61 TTKDVIQGISVGDLLGVGPFPGGALVSPYTNFLNTIMPSEDPWKAFMQVVALMDQK 120
QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFRNS 180
Db 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFRNS 180
QY 181 MPFSAISGYEVLFTTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
Db 181 MPFSAISGYEVLFTTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
QY 241 DHCKWYNVGLDKLGGSSYESWVNFNRYRREMTLTVDLIALPPLYDVRLYPKVEKTELT 300
Db 241 DHCKWYNVGLDKLGGSSYESWVNFNRYRREMTLTVDLIALPPLYDVRLYPKVEKTELT 300
QY 301 RDVLTDPVGVNNLRGCTFESNIENYIRKPHLEFDYLRHIOFHRRFOPGYGNDSEFNWS 360
Db 301 RDVLTDPVGVNNLRGCTFESNIENYIRKPHLEFDYLRHIOFHRRFOPGYGNDSEFNWS 360
QY 361 GNYVSTRPSIGSNDIITSPEYGNKSSBPVONLEFNGEKYRAVANNTLAVMPSAVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPEYGNKSSBPVONLEFNGEKYRAVANNTLAVMPSAVYSGVT 420
QY 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNTYWCFL 480
Db 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNTYWCFL 480
QY 481 MGSRGITPVLWTMHSVDFEENMIDSKKITQLPLVKAKYKQSGASVAVAGRPFTGCDIIOC 540
Db 481 MGSRGITPVLWTMHSVDFEENMIDSKKITQLPLVKAKYKQSGASVAVAGRPFTGCDIIOC 540
QY 541 TENGSAATVYTPDVYSOKYRARIHYASTQITFTLSLDGAPPNQYFEDKTINKGDTLT 600
Db 541 TENGSAATVYTPDVYSOKYRARIHYASTQITFTLSLDGAPPNQYFEDKTINKGDTLT 600
QY 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFIPVN 644
Db 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFIPVN 644

```

```

RESULT 5
US-09-027-998A-2
; Sequence 2, Application US/09027998A
; Patent No. 6284949
; GENERAL INFORMATION:
; APPLICANT: Flaschoff, David A
; APPLICANT: Fuchs, Roy L
; TITLE OF INVENTION: Insect Resistant Plants
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White and Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,998A
; FILING DATE: 23-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT.195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; INFORMATION FOR SEQ ID NO: 2:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 644 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-09-027-998A-2

```

```

Query Match 100.0%; Score 644; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDNANTKEFLBMTADNNTALDSS 60
Db 1 MNPNNRSEHDITKTENNEVPTNHQYPLAETPNPTLEDNANTKEFLBMTADNNTALDSS 60
QY 61 TTKDVIQGISVGDLLGVGPFPGGALVSPYTNFLNTIMPSEDPWKAFMQVVALMDQK 120
Db 61 TTKDVIQGISVGDLLGVGPFPGGALVSPYTNFLNTIMPSEDPWKAFMQVVALMDQK 120
QY 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFRNS 180
Db 121 IADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSQAESHPFRNS 180
QY 181 MPFSAISGYEVLFTTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
Db 181 MPFSAISGYEVLFTTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
QY 241 DHCKWYNVGLDKLGGSSYESWVNFNRYRREMTLTVDLIALPPLYDVRLYPKVEKTELT 300
Db 241 DHCKWYNVGLDKLGGSSYESWVNFNRYRREMTLTVDLIALPPLYDVRLYPKVEKTELT 300
QY 301 RDVLTDPVGVNNLRGCTFESNIENYIRKPHLEFDYLRHIOFHRRFOPGYGNDSEFNWS 360
Db 301 RDVLTDPVGVNNLRGCTFESNIENYIRKPHLEFDYLRHIOFHRRFOPGYGNDSEFNWS 360
QY 361 GNYVSTRPSIGSNDIITSPEYGNKSSBPVONLEFNGEKYRAVANNTLAVMPSAVYSGVT 420
Db 361 GNYVSTRPSIGSNDIITSPEYGNKSSBPVONLEFNGEKYRAVANNTLAVMPSAVYSGVT 420
QY 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNTYWCFL 480
Db 421 KVEFSQYNDQDEASTQYDSKRNVGAVSWDSIDQLPETTDEPLEKGYSHQNTYWCFL 480
QY 481 MGSRGITPVLWTMHSVDFEENMIDSKKITQLPLVKAKYKQSGASVAVAGRPFTGCDIIOC 540
Db 481 MGSRGITPVLWTMHSVDFEENMIDSKKITQLPLVKAKYKQSGASVAVAGRPFTGCDIIOC 540
QY 541 TENGSAATVYTPDVYSOKYRARIHYASTQITFTLSLDGAPPNQYFEDKTINKGDTLT 600
Db 541 TENGSAATVYTPDVYSOKYRARIHYASTQITFTLSLDGAPPNQYFEDKTINKGDTLT 600
QY 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFIPVN 644
Db 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFIPVN 644

```

```

RESULT 6
PCT-US92-11337-4
; Sequence 4, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIMANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:

```


MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337
FILING DATE: 19921231
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
AMPHIPHILIC: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: NIGRIENSIS
INDIVIDUAL ISOLATE: PS40D1
IMMEDIATE SOURCE:
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF FRANK GAERTNER
CLONE: 40D1
PCT-US92-11337-4

Query Match 100.0%; Score 644; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNTKEFLRMADNNTALDSS 60
1 MNPNNSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNTKEFLRMADNNTALDSS 60
61 TTRDVIOKGISVGGDLGVGPFPGALVSFTNFTLNTIWPSEDPWKAEMEVEALMDOK 120
61 TTRDVIOKGISVGGDLGVGPFPGALVSFTNFTLNTIWPSEDPWKAEMEVEALMDOK 120
121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSSQAESHRMS 180
121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSSQAESHRMS 180
121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSSQAESHRMS 180
181 MPSPAIISGYEVLFTTYVAOANTHFLFKDAQTYGEEGMEKEDIAEFYKROKLQOET 240
181 MPSPAIISGYEVLFTTYVAOANTHFLFKDAQTYGEEGMEKEDIAEFYKROKLQOET 240
181 MPSPAIISGYEVLFTTYVAOANTHFLFKDAQTYGEEGMEKEDIAEFYKROKLQOET 240
241 DHCKVKNVAGDLKRGSSYSWVNFNRYRREMTLVLDLALFPLVDRLYPREVKTELT 300
241 DHCKVKNVAGDLKRGSSYSWVNFNRYRREMTLVLDLALFPLVDRLYPREVKTELT 300
301 RDVITDPIVGVNRLRGCTFNSNENTIRKPHLFYHRIQFPHRPGGYGNDSEFYMS 360
301 RDVITDPIVGVNRLRGCTFNSNENTIRKPHLFYHRIQFPHRPGGYGNDSEFYMS 360
301 RDVITDPIVGVNRLRGCTFNSNENTIRKPHLFYHRIQFPHRPGGYGNDSEFYMS 360
361 GNYSTRPSIGSNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 420
361 GNYSTRPSIGSNDIITSPEYGNKSEPVONLEFNGEKYRAVANNTLAWPMSAVYSGVT 420
421 KVEFSQINDOTDEASTQYTSKRNVGAVSWDSIDQLPEPTDEPLEKGYSHQLNLYVWCF 480
421 KVEFSQINDOTDEASTQYTSKRNVGAVSWDSIDQLPEPTDEPLEKGYSHQLNLYVWCF 480
481 MGSRGITPVLWTNHSVDPEFNMIDSKKITQPLVYKAYKLGSGASVAVAGRFPGGDIIOC 540

|||||
481 MGSRGITPVLWTNHSVDPEFNMIDSKKITQPLVYKAYKLGSGASVAVAGRFPGGDIIOC 540
541 TENGSAATITVYPDVYSQKYRARIHYASTSQITFTLSLDGAPFNOYFEDTINKGDTLT 600
541 TENGSAATITVYPDVYSQKYRARIHYASTSQITFTLSLDGAPFNOYFEDTINKGDTLT 600
601 YNSFNLASFTPELPGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
601 YNSFNLASFTPELPGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644

RESULT 7
US-08-996-441B-113
Sequence 113, Application US/08996441B
Patent No. 6023013
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brusock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MEOC-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-996-441B-113

Query Match 100.0%; Score 644; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNTKEFLRMADNNTALDSS 60
1 MNPNNSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNTKEFLRMADNNTALDSS 60
9 MNPNNSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNTKEFLRMADNNTALDSS 68
61 TTRDVIOKGISVGGDLGVGPFPGALVSFTNFTLNTIWPSEDPWKAEMEVEALMDOK 120
61 TTRDVIOKGISVGGDLGVGPFPGALVSFTNFTLNTIWPSEDPWKAEMEVEALMDOK 120
69 TTRDVIOKGISVGGDLGVGPFPGALVSFTNFTLNTIWPSEDPWKAEMEVEALMDOK 128
121 IADYAKKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSOGRIRELFSSQAESHRMS 180

```

Db 129 IADYAKNKALAELOGLONNEDYVSALSSWQKNPVSSRNPHSOGRIELEFSQAESHPFRNS 188
QY 181 MPSPAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
Db 189 MPSPAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 248
QY 241 DHCYKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLYDVRLYPKKEVKTFLT 300
Db 249 DHCYKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLYDVRLYPKKEVKTFLT 308
QY 301 RDVLTDPIYGVNVLRGYGTFSNENIYRKPHLFDYLAHRIOPHRRPOGYGNDSEFWYMS 360
Db 309 RDVLTDPIYGVNVLRGYGTFSNENIYRKPHLFDYLAHRIOPHRRPOGYGNDSEFWYMS 368
QY 361 GNVYSTRPSIGSNDIITSPFYGNKSSRPYONLEFNGEKYRAVANNTMLAVMPASVYSGVT 420
Db 369 GNVYSTRPSIGSNDIITSPFYGNKSSRPYONLEFNGEKYRAVANNTMLAVMPASVYSGVT 428
QY 421 KVEFSQYNDQTDASTQYTSKRNVGAVSMDSIDQLPETTDEPLEKGYSHQNLVWMCFL 480
Db 429 KVEFSQYNDQTDASTQYTSKRNVGAVSMDSIDQLPETTDEPLEKGYSHQNLVWMCFL 488
QY 481 MGSRGITPVLWTWTKSVDFENMIDSKKITQPLVKAYKLOSASVAVAGPRTGGDIIOC 540
Db 489 MGSRGITPVLWTWTKSVDFENMIDSKKITQPLVKAYKLOSASVAVAGPRTGGDIIOC 548
QY 541 TENGSAATIVYTPDVYSQYRARIHVASTQITFTLSLDGAPFNQYFDDTKINKGDTLT 600
Db 549 TENGSAATIVYTPDVYSQYRARIHVASTQITFTLSLDGAPFNQYFDDTKINKGDTLT 608
QY 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFTIPVN 644
Db 609 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFTIPVN 652

```

RESULT 8
US-08-993-722A-113
Sequence 113, Application US/08993722A
Patent No. 6060594
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terssch, Michael A.
TITLE OF INVENTION: NUCLEIC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: COLLECTORAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993/722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MEOO:149
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-722A-113
Query Match 100.0%; Score 644; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNSEDDITKTNNNEVPNNHVOYPLAETPNPTLEDNANKEFLRMADNNEALSS 60
Db 9 MNPNNSEDDITKTNNNEVPNNHVOYPLAETPNPTLEDNANKEFLRMADNNEALSS 68
QY 61 TTKDVIQKISVVGDLGIVGFPFGALVSFTNPLNTIWPSEDPKAFMEQVEALMDQK 120
Db 69 TTKDVIQKISVVGDLGIVGFPFGALVSFTNPLNTIWPSEDPKAFMEQVEALMDQK 128
QY 121 IADYAKNKALAELOGLONNEDYVSALSSWQKNPVSSRNPHSOGRIELEFSQAESHPFRNS 180
Db 129 IADYAKNKALAELOGLONNEDYVSALSSWQKNPVSSRNPHSOGRIELEFSQAESHPFRNS 188
QY 181 MPSPAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 240
Db 189 MPSPAISGEVLFLLTYAAQANTHLFLKDAQIYGEEMGYEKEDIAEFYKROLKLTQOBYT 248
QY 241 DHCYKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLYDVRLYPKKEVKTFLT 300
Db 249 DHCYKWNVGLDKLRGSSYSWVNFNRRREMTLTVLDLALFPLYDVRLYPKKEVKTFLT 308
QY 301 RDVLTDPIYGVNVLRGYGTFSNENIYRKPHLFDYLAHRIOPHRRPOGYGNDSEFWYMS 360
Db 309 RDVLTDPIYGVNVLRGYGTFSNENIYRKPHLFDYLAHRIOPHRRPOGYGNDSEFWYMS 368
QY 361 GNVYSTRPSIGSNDIITSPFYGNKSSRPYONLEFNGEKYRAVANNTMLAVMPASVYSGVT 420
Db 369 GNVYSTRPSIGSNDIITSPFYGNKSSRPYONLEFNGEKYRAVANNTMLAVMPASVYSGVT 428
QY 421 KVEFSQYNDQTDASTQYTSKRNVGAVSMDSIDQLPETTDEPLEKGYSHQNLVWMCFL 480
Db 429 KVEFSQYNDQTDASTQYTSKRNVGAVSMDSIDQLPETTDEPLEKGYSHQNLVWMCFL 488
QY 481 MGSRGITPVLWTWTKSVDFENMIDSKKITQPLVKAYKLOSASVAVAGPRTGGDIIOC 540
Db 489 MGSRGITPVLWTWTKSVDFENMIDSKKITQPLVKAYKLOSASVAVAGPRTGGDIIOC 548
QY 541 TENGSAATIVYTPDVYSQYRARIHVASTQITFTLSLDGAPFNQYFDDTKINKGDTLT 600
Db 549 TENGSAATIVYTPDVYSQYRARIHVASTQITFTLSLDGAPFNQYFDDTKINKGDTLT 608
QY 601 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFTIPVN 644
Db 609 YNSFNLASFTPELSCNNLQIGVTGLSAGDKYIYDKIEFTIPVN 652

```

RESULT 9
US-08-993-170A-113
Sequence 113, Application US/08993170A
Patent No. 6063597
GENERAL INFORMATION:
APPLICANT: English, Leigh H.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Terssch, Michael A.
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO

TITLE OF INVENTION: COLEOPTERAN INSECTS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/993,170A
 FILING DATE: 18-DEC-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: MECO:002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 652 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-993-170A-113

Query Match 100.0%; Score 644; DB 3; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNRSEHDITKTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMATADNNTALDSS 60
 9 MNPNNRSEHDITKTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMATADNNTALDSS 68
 61 TTKDVIQKGISVYDGLGVGPFEGALVSFTYTNPLNTIMPSEDPKAFMEOVEALMDOK 120
 69 TTKDVIQKGISVYDGLGVGPFEGALVSFTYTNPLNTIMPSEDPKAFMEOVEALMDOK 128
 121 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSQGRIRLFSQAESHPFNS 180
 129 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSQGRIRLFSQAESHPFNS 188
 181 MPFALISGEVLEFLLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQET 240
 189 MPFALISGEVLEFLLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQET 248
 241 DHCVKRYNYGDLKLGSSYSESVNPNRYRREMTLVLDLALFPLDYRLPKKVEKTELT 300
 249 DHCVKRYNYGDLKLGSSYSESVNPNRYRREMTLVLDLALFPLDYRLPKKVEKTELT 308
 301 RDVLTPDIYGVNNLNGYGTTFNSNIENYIRKPHLFYLRHIOFHTRFQGYGNDSEFNWS 360
 309 RDVLTPDIYGVNNLNGYGTTFNSNIENYIRKPHLFYLRHIOFHTRFQGYGNDSEFNWS 368
 361 GNVYSTRPSIGSDITTSFYGNKSEPEYONLEFNGEKYRANVTNLAVMPSAVYSGVT 420
 369 GNVYSTRPSIGSDITTSFYGNKSEPEYONLEFNGEKYRANVTNLAVMPSAVYSGVT 428
 421 KVEFSYONDOTDASTOTYDSKRNVAGVMSDIDLPETTDEPLEKGYSHOANTVMCFL 480
 429 KVEFSYONDOTDASTOTYDSKRNVAGVMSDIDLPETTDEPLEKGYSHOANTVMCFL 488
 481 MGSRGITPVLWTHRSVDFENMIDSKKITTQLPLVKAAYLQSGASVAGPRTGGDIIOC 540
 489 MGSRGITPVLWTHRSVDFENMIDSKKITTQLPLVKAAYLQSGASVAGPRTGGDIIOC 548

QY 541 TENGSAATIVTPDVDSQYKRYRARIHYASTQITTLSDGAPFNOYFEDKTINKGDTLT 600
 DB 549 TENGSAATIVTPDVDSQYKRYRARIHYASTQITTLSDGAPFNOYFEDKTINKGDTLT 608
 QY 601 YNSFNLASFSTPELGSNNIOLIGVTGLSAGDKYIDKIEFIYVN 644
 DB 609 YNSFNLASFSTPELGSNNIOLIGVTGLSAGDKYIDKIEFIYVN 652

RESULT 10

US-08-993-775B-113

Sequence 113, Application US/08993775B

Patent No. 6077824

GENERAL INFORMATION:

APPLICANT: English, Leigh H.

APPLICANT: Brusock, Susan M.

APPLICANT: Malvar, Thomas M.

APPLICANT: Bryson, James W.

APPLICANT: Kulesza, Caroline A.

APPLICANT: Walters, Frederick S.

APPLICANT: Slatin, Stephen L.

APPLICANT: Von Tersch, Michael A.

TITLE OF INVENTION: METHODS FOR IMPROVING THE ACTIVITY OF

DELTA-ENDOTOXINS AGAINST INSECT PESTS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,775B

FILING DATE: 18-DEC-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: MECO:150

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 652 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-993-775B-113

Query Match 100.0%; Score 644; DB 3; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNNRSEHDITKTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMATADNNTALDSS 60
 9 MNPNNRSEHDITKTENNNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMATADNNTALDSS 68
 61 TTKDVIQKGISVYDGLGVGPFEGALVSFTYTNPLNTIMPSEDPKAFMEOVEALMDOK 120
 69 TTKDVIQKGISVYDGLGVGPFEGALVSFTYTNPLNTIMPSEDPKAFMEOVEALMDOK 128
 121 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSQGRIRLFSQAESHPFNS 180
 129 IADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSQGRIRLFSQAESHPFNS 188
 181 MPFALISGEVLEFLLTYAQAANTHLFLKDAQIYGEEMGYEKEDIAEFYKRLKLTQET 240

```

Db 189 MPSEFISGEVLEFLTYAQAANTHLFLKDAQITGEEGKEKEDIAEFYKROKLQEXT 248
QY 241 DHCVKAVNGDLKRGSSYESVWVFNFRREMLTVLDLALPLVDVRLYREVTTELT 300
Db 249 DHCKVAVNGDLKRGSSYESVWVFNFRREMLTVLDLALPLVDVRLYREVTTELT 308
QY 301 RDVLTPDIVGNVNLRGYGTTFNSNIENYIRKPHLEFDYLRHQFTRPQPGYGNDSFNYS 360
Db 309 RDVLTPDIVGNVNLRGYGTTFNSNIENYIRKPHLEFDYLRHQFTRPQPGYGNDSFNYS 368
QY 361 GNVYSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 420
Db 369 GNVYSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTNLAVMPSAVYSGVT 428
QY 421 KVEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPTTEDEPLEKGSYHOLNVMCL 480
Db 429 KVEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPTTEDEPLEKGSYHOLNVMCL 488
QY 481 MGSRCITPVLWTHKSVDFPNMIDSKKITQLPLVYKAYLQSGASVAGPRTGGDIQC 540
Db 489 MGSRCITPVLWTHKSVDFPNMIDSKKITQLPLVYKAYLQSGASVAGPRTGGDIQC 548
QY 541 TENGSAATIVTPDVSYSOQRARIHASTSQTITFLSIDGAPFNOYFDDKTINKGDTLT 600
Db 549 TENGSAATIVTPDVSYSOQRARIHASTSQTITFLSIDGAPFNOYFDDKTINKGDTLT 608
QY 601 YNSFNLASSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 609 YNSFNLASSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 652

```

RESULT 11

```

US-08-704-966-2
; Sequence 2, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rochelleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sallwanchik, Lloyd & Sallwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,966
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:

```

```

NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MPS 8-88ARD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-704-966-2

```

```

Query Match 92.7%; Score 597; DB 3; Length 597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 48 MTADNTEALDSSTTDVYQKISVVGDLGVYFPPGALVSFYTNFLNTIMSEDPWK 107
Db 1 MTADNTEALDSSTTDVYQKISVVGDLGVYFPPGALVSFYTNFLNTIMSEDPWK 60
QY 108 AFMEQVEALMDOKIADYAKKALAELOGLNNVEDYVGLSWMCKNRYSSRNPSQKIR 167
Db 61 AFMEQVEALMDOKIADYAKKALAELOGLNNVEDYVGLSWMCKNRYSSRNPSQKIR 120
QY 168 ELFSQAESHFRRNSMPSFAISGYEVLFTTYAQAANTHLFLKDAQITGEEGKEKEDIAE 227
Db 121 ELFSQAESHFRRNSMPSFAISGYEVLFTTYAQAANTHLFLKDAQITGEEGKEKEDIAE 180
QY 228 FYKROLKTOEYTDHCYKMYNGLDKLGRSSYESVWVFNFRREMLTVLDLALPLVD 287
Db 181 FYKROLKTOEYTDHCYKMYNGLDKLGRSSYESVWVFNFRREMLTVLDLALPLVD 240
QY 288 VRLYREVTTELTRDVLDPDIVGNVNLRGYGTTFNSNIENYIRKPHLEFDYLRHQFTRPQ 347
Db 241 VRLYREVTTELTRDVLDPDIVGNVNLRGYGTTFNSNIENYIRKPHLEFDYLRHQFTRPQ 300
QY 348 PGYGNDSFNYSGNVYSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTN 407
Db 301 PGYGNDSFNYSGNVYSTRPSIGSNDITSPRYGKSSSPVQNLFEENGKYYRAVANTN 360
QY 408 LAVMPSAVYSGVTKEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPTTEDEPLEK 467
Db 361 LAVMPSAVYSGVTKEFSQYNDQDEASTQYDYSKRNNGAVSWSIDQLPPTTEDEPLEK 420
QY 468 GYSHOLNVMCLMGSRCITPVLWTHKSVDFPNMIDSKKITQLPLVYKAYLQSGASVY 527
Db 421 GYSHOLNVMCLMGSRCITPVLWTHKSVDFPNMIDSKKITQLPLVYKAYLQSGASVY 480
QY 528 AGPRTGGDIQCTENGSAATIVTPDVSYSOQRARIHASTSQTITFLSIDGAPFNOY 587
Db 481 AGPRTGGDIQCTENGSAATIVTPDVSYSOQRARIHASTSQTITFLSIDGAPFNOY 540
QY 588 YFDKTINKGDTLTYNSFNLASSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 644
Db 541 YFDKTINKGDTLTYNSFNLASSTPELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN 597

```

RESULT 12

```

US-08-705-438-2
; Sequence 2, Application US/08705438
; Patent No. 6015891
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rochelleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Salliwanchik, Lloyd & Salliwanchik
 STREET: 1000 Legion Place, Suite 1750
 CITY: Orlando
 STATE: Florida
 COUNTRY: USA
 ZIP: 32801
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/705,438
 FILING DATE: 29-AUG-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/369,839
 FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFD4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 597 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-705-438-2

Query Match 92.7%; Score 597; DB 3; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MTADNNTALDSSTTKDYIOKGISVGDLLGVGFFPGGALVSYTFLNTIMPSEDPK 107
 DB 1 MTADNNTALDSSTTKDYIOKGISVGDLLGVGFFPGGALVSYTFLNTIMPSEDPK 60
 QY 108 AFMEQVEALMDOKIADYAKNKALAELOGLQNNVEDYVSALSSMOKNPNVSSRNPHSQRIR 167
 DB 61 AFMEQVEALMDOKIADYAKNKALAELOGLQNNVEDYVSALSSMOKNPNVSSRNPHSQRIR 120
 QY 168 ELFSQAESHFNRSMPSFAISGTEVLFLLTYAOANTHLFLKDKQIYGEENGKEKIDAE 227
 DB 121 ELFSQAESHFNRSMPSFAISGTEVLFLLTYAOANTHLFLKDKQIYGEENGKEKIDAE 180
 QY 228 FFKRDLKLTQOETDHCVKWYNVGLDKLGSSYESVWNNFRYRREMTLVLDLALFLPLYD 287
 DB 181 FFKRDLKLTQOETDHCVKWYNVGLDKLGSSYESVWNNFRYRREMTLVLDLALFLPLYD 240
 QY 288 VRLYPRVETELRDVLDPIVGVNNLQGYTTFESNIENYLRKPLFDYLRHQFHTRFQ 347
 DB 241 VRLYPRVETELRDVLDPIVGVNNLQGYTTFESNIENYLRKPLFDYLRHQFHTRFQ 300
 QY 348 PGYGGDSFNYSNGVYSTRPSISGNDITTSFYGNKSSEPQNLFEENGKRYRAVANTN 407
 DB 301 PGYGGDSFNYSNGVYSTRPSISGNDITTSFYGNKSSEPQNLFEENGKRYRAVANTN 360
 QY 408 LAVPAPVSGVYKEFEFSQYNDQTDASTQTYDSKRNVGAVSWSDIDLPPETTDEPLEK 467

DB 361 LAVPAPVSGVYKEFEFSQYNDQTDASTQTYDSKRNVGAVSWSDIDLPPETTDEPLEK 420
 QY 468 GYSHQNLVWYCFMLOGSRGTIPVLTWTHKSVDFPNMIDSKITQOLPVKAYKLOGSASV 527
 DB 421 GYSHQNLVWYCFMLOGSRGTIPVLTWTHKSVDFPNMIDSKITQOLPVKAYKLOGSASV 480
 QY 528 AGPFTGGDIIOCTENGSAATIVYPDVYSOKYRARIHYASTQITTLSDGAPFNOY 587
 DB 481 AGPFTGGDIIOCTENGSAATIVYPDVYSOKYRARIHYASTQITTLSDGAPFNOY 540
 QY 588 YPFTIKKGDITLYNSFNLFASFPELGGNNLQIGVGLSAGDVKYIDKIEFIPVN 644
 DB 541 YPFTIKKGDITLYNSFNLFASFPELGGNNLQIGVGLSAGDVKYIDKIEFIPVN 597

RESULT 13
 US-08-704-966-4
 Sequence 4, Application US/08704966
 Patent No. 601523
 GENERAL INFORMATION:
 APPLICANT: Adang, Michael J.
 APPLICANT: Rocheleau, Thomas A.
 APPLICANT: Merlo, Donald
 APPLICANT: Murray, Elizabeth E.
 TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Salliwanchik, Lloyd & Salliwanchik
 STREET: 1000 Legion Place, Suite 1750
 CITY: Orlando
 STATE: Florida
 COUNTRY: USA
 ZIP: 32801
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/704,966
 FILING DATE: 29-AUG-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/369,839
 FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-704-966-4

Query Match 92.4%; Score 595; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 595: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSSTTKVDYIQKISVVDLLGVGFPGCALVSFTYNTFNTIMPSEDPMKAF 109
 DB 3 ADNNTALDSSSTTKVDYIQKISVVDLLGVGFPGCALVSFTYNTFNTIMPSEDPMKAF 62

QY 110 MEQVEALMDQKIDYAKKAKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGGRIRREL 169
 DB 63 MEQVEALMDQKIDYAKKAKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGGRIRREL 122

QY 170 FSOAESHFNRSMPSFAISGYEVLFTTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 229
 DB 123 FSOAESHFNRSMPSFAISGYEVLFTTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 182

QY 230 KRQLKLTQETDHCYKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLDYVR 289
 DB 183 KRQLKLTQETDHCYKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLDYVR 242

QY 290 LYRKVEKTELTRDVLTPDIYGVNNLRGVTGTSNTIENTYIKRPHLDYLRHQFTFRQPG 349
 DB 243 LYRKVEKTELTRDVLTPDIYGVNNLRGVTGTSNTIENTYIKRPHLDYLRHQFTFRQPG 302

QY 350 YYGNDSPFNWGSNGYVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANNTLA 409
 DB 303 YYGNDSPFNWGSNGYVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANNTLA 362

QY 410 VMPASVYSGVTKEVSQYNDOTDEASTQYDSCRNVGAVSWDSIDQLPETTDEPLEKGY 469
 DB 363 VMPASVYSGVTKEVSQYNDOTDEASTQYDSCRNVGAVSWDSIDQLPETTDEPLEKGY 422

QY 470 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKRTIQLPLVAKYKQSGASVYAG 529
 DB 423 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKRTIQLPLVAKYKQSGASVYAG 482

QY 530 PRFTGGDIIOCTENGSAATYVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYF 589
 DB 483 PRFTGGDIIOCTENGSAATYVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYF 542

QY 590 DKTINKGDTLTVNSFNLASFTPELSSGNNOIGVTGLSAGDKYIDKIEPIPVN 644
 DB 543 DKTINKGDTLTVNSFNLASFTPELSSGNNOIGVTGLSAGDKYIDKIEPIPVN 597

RESULT 14
 US-08-705-438-4
 ; Sequence 4, Application US/08705438
 ; Patent No. 6015891
 ; GENERAL INFORMATION:
 ; APPLICANT: Adang, Michael J.
 ; APPLICANT: Rochelleau, Thomas A.
 ; APPLICANT: Merlo, Donald
 ; APPLICANT: Murray, Elizabeth E.
 ; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik
 ; STREET: 1000 Legion Place, Suite 1750
 ; CITY: Orlando
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32801
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,438
 ; FILING DATE: 29-AUG-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/369,839

FILING DATE: 06-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,191
 FILING DATE: 03-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,844
 FILING DATE: 28-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/242,482
 FILING DATE: 09-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MPS 8-88AFDA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 407-426-7500
 TELEFAX: 407-839-8589
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-705-438-4

Query Match 92.4%; Score 595; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 595: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSSSTTKVDYIQKISVVDLLGVGFPGCALVSFTYNTFNTIMPSEDPMKAF 109
 DB 3 ADNNTALDSSSTTKVDYIQKISVVDLLGVGFPGCALVSFTYNTFNTIMPSEDPMKAF 62

QY 110 MEQVEALMDQKIDYAKKAKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGGRIRREL 169
 DB 63 MEQVEALMDQKIDYAKKAKALAELOGLONNVEDYVSALSSWQKNPVSSRNPHSGGRIRREL 122

QY 170 FSOAESHFNRSMPSFAISGYEVLFTTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 229
 DB 123 FSOAESHFNRSMPSFAISGYEVLFTTYAOAANTHLFLKDAQITGEEGKEKEDIAEFY 182

QY 230 KRQLKLTQETDHCYKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLDYVR 289
 DB 183 KRQLKLTQETDHCYKMYNGLDKLRGSSYESWVNFNRYRREMTLVLDLALFPLDYVR 242

QY 290 LYRKVEKTELTRDVLTPDIYGVNNLRGVTGTSNTIENTYIKRPHLDYLRHQFTFRQPG 349
 DB 243 LYRKVEKTELTRDVLTPDIYGVNNLRGVTGTSNTIENTYIKRPHLDYLRHQFTFRQPG 302

QY 350 YYGNDSPFNWGSNGYVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANNTLA 409
 DB 303 YYGNDSPFNWGSNGYVSTRPSIGSNDITSPFYGNKSEPVONLEFNGEKYRAVANNTLA 362

QY 410 VMPASVYSGVTKEVSQYNDOTDEASTQYDSCRNVGAVSWDSIDQLPETTDEPLEKGY 469
 DB 363 VMPASVYSGVTKEVSQYNDOTDEASTQYDSCRNVGAVSWDSIDQLPETTDEPLEKGY 422

QY 470 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKRTIQLPLVAKYKQSGASVYAG 529
 DB 423 SHOANVMCFMLQSGKRTIPVLTWTHKSVDFNMDSKRTIQLPLVAKYKQSGASVYAG 482

QY 530 PRFTGGDIIOCTENGSAATYVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYF 589
 DB 483 PRFTGGDIIOCTENGSAATYVTPDVYSQYRARIHYASTQITFTLSLDGAPFNQYF 542

QY 590 DKTINKGDTLTVNSFNLASFTPELSSGNNOIGVTGLSAGDKYIDKIEPIPVN 644
 DB 543 DKTINKGDTLTVNSFNLASFTPELSSGNNOIGVTGLSAGDKYIDKIEPIPVN 597

RESULT 15
 US-08-295-060-4

; Sequence 4, Application US/08295060
; Patent No. 5659123
; GENERAL INFORMATION:
; APPLICANT: VAN RIE, Jeroen
; APPLICANT: JANSSENS, Stefan
; APPLICANT: PEREROEN, Martin
; TITLE OF INVENTION: NEW DIABROTICA TOXINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,060
; FILING DATE: 26-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; US-08-295-060-4

Query Match 53.4%; Score 344; DB 1; Length 645;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NPNNSEHDTIKTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTALDSST 61
DB 3 NPNNSEHDTIKTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADNNTALDSST 62
QY 62 TKDVIQKGISVVGDLGAVGFPFGGALVSFTYTNFLNTIWPSEDPKAFMEQVEALMDOKI 121
DB 63 TKDVIQKGISVVGDLGAVGFPFGGALVSFTYTNFLNTIWPSEDPKAFMEQVEALMDOKI 122
QY 122 ADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSGRIRELFSQASHFRNSM 181
DB 123 ADYAKNKALAELOGLONNVEDYVSALSSMOKNPVSSRNPHSGRIRELFSQASHFRNSM 182
QY 182 PSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYTD 241
DB 183 PSFAISGEVLEFLTYAQAANTHFLKDAQIYGEEMGEKEDIAEFYKROLKLTQEYTD 242
QY 242 HCVKKNVNGDLKRGSSYSVSVNFRNRYRREMTLVLDLALPPLYDVRLYPREVKTELTR 301
DB 243 HCVKKNVNGDLKRGSSYSVSVNFRNRYRREMTLVLDLALPPLYDVRLYPREVKTELTR 302
QY 302 DVLTPDIVGVNMLRGYGTFSNIENYIRKPHLFDYLRHIOFHTR 345
DB 303 DVLTPDIVGVNMLRGYGTFSNIENYIRKPHLFDYLRHIOFHTR 346

Search completed: January 10, 2003, 11:11:25
Job time : 17 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:09:35 : Search time 11 Seconds
(without alignments)
1135.844 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MNPNNRSEHDITKTENNNEV.....TGLSGADKYIKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 118974 seqs, 19401057 residues

Word size: 0
Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCRT_NEM_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCRTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	644	US-09-943-692-2	Sequence 2, Appl
2	20	3.1	20	US-09-943-692-3	Sequence 53, Appl
3	15	2.3	15	US-09-943-692-3	Sequence 3, Appl
4	12	1.9	12	US-09-943-692-47	Sequence 47, Appl
5	12	1.9	12	US-09-943-692-50	Sequence 50, Appl
6	11	1.7	11	US-09-943-692-26	Sequence 26, Appl
7	11	1.7	11	US-10-032-717-18	Sequence 8, Appl
8	10	1.6	10	US-10-032-717-18	Sequence 18, Appl
9	10	1.6	10	US-10-032-717-4	Sequence 4, Appl
10	10	1.6	10	US-10-120-544A-18	Sequence 18, Appl
11	10	1.6	10	US-10-120-544A-6	Sequence 6, Appl
12	10	1.6	10	US-10-120-544A-18	Sequence 31, Appl
13	9	1.4	9	US-09-738-363-31	Sequence 31, Appl
14	8	1.2	8	US-09-943-692-29	Sequence 29, Appl
15	8	1.2	8	US-09-943-692-20	Sequence 20, Appl
16	8	1.2	8	US-09-864-761-44452	Sequence 44452, A
17	7	1.1	7	US-09-796-692-1601	Sequence 1601, Ap
18	7	1.1	7	US-09-796-692-1962	Sequence 1962, Ap
19	7	1.1	7	US-09-796-692-2485	Sequence 2485, Ap

20	7	1.1	157	10	US-09-816-669A-2	Sequence 2, Appl
21	7	1.1	327	10	US-09-886-055-249	Sequence 249, App
22	7	1.1	485	9	US-09-712-363-208	Sequence 208, App
23	7	1.1	616	12	US-10-032-717-20	Sequence 20, Appl
24	7	1.1	617	12	US-10-032-717-34	Sequence 34, Appl
25	7	1.1	617	12	US-10-032-717-46	Sequence 46, Appl
26	7	1.1	620	12	US-10-032-717-30	Sequence 30, Appl
27	7	1.1	620	12	US-10-032-717-32	Sequence 32, Appl
28	7	1.1	620	12	US-10-032-717-42	Sequence 42, Appl
29	7	1.1	637	10	US-09-852-053-3	Sequence 3, Appl
30	7	1.1	643	10	US-09-826-660-25	Sequence 25, Appl
31	7	1.1	644	9	US-09-738-626-5330	Sequence 5330, Ap
32	7	1.1	667	12	US-10-032-717-6	Sequence 6, Appl
33	7	1.1	669	12	US-10-032-717-10	Sequence 16, Appl
34	7	1.1	669	12	US-10-032-717-16	Sequence 16, Appl
35	7	1.1	670	12	US-10-032-717-24	Sequence 24, Appl
36	7	1.1	670	12	US-10-032-717-44	Sequence 44, Appl
37	7	1.1	673	12	US-10-032-717-12	Sequence 12, Appl
38	7	1.1	673	12	US-10-032-717-22	Sequence 22, Appl
39	7	1.1	673	12	US-10-032-717-40	Sequence 40, Appl
40	7	1.1	673	12	US-10-032-717-40	Sequence 334, App
41	7	1.1	791	10	US-09-881-752A-334	Sequence 5208, Ap
42	7	1.1	892	9	US-09-738-626-5208	Sequence 4, Appl
43	7	1.1	1109	10	US-09-756-526A-4	Sequence 2, Appl
44	7	1.1	1163	10	US-09-756-526A-2	Sequence 23, Appl
45	7	1.1	1186	10	US-09-826-660-23	Sequence 2, Appl
			1206	12	US-10-032-717-2	

ALIGNMENTS

RESULT 1
US-09-943-692-2
Sequence 2, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAYRIK, PAUL B.
APPLICANT: McPHERSON, SYLVIA A.
APPLICANT: PERLAR, FREDERICK J.
TITLE OF INVENTION: COLDOPEPERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195-1
CURRENT APPLICATION NUMBER: US/09/943, 692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027, 998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 644
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-2

Query Match
Best Local Similarity 100.0%; Score 644; DB 10; Length 644;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDITKTENNNEVPNNHOYPLAEPTLTEDLNKKEFLRATDNNTEALDSS 60
DB 1 MNPNNRSEHDITKTENNNEVPNNHOYPLAEPTLTEDLNKKEFLRATDNNTEALDSS 60
QY 61 TTKDVYOKGIVSYVDLGVVGFPGFALVSEFTNPLNTIWPSEDPWAKFMQVEALNDK 120
DB 61 TTKDVYOKGIVSYVDLGVVGFPGFALVSEFTNPLNTIWPSEDPWAKFMQVEALNDK 120
QY 121 IADYAKKALAELOGLQNNVEDYVSLSSWQKNPVSRRPHSGRIRLFQASHEHFRNS 180
DB 121 IADYAKKALAELOGLQNNVEDYVSLSSWQKNPVSRRPHSGRIRLFQASHEHFRNS 180

```

QY 101 MPSPASISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROKLTQOET 240
DB 101 MPSPASISGYEVLFTTYAQAANTHLFLKDAQIYGEEMGEKEDIAEFYKROKLTQOET 240
QY 241 DHCVAVYWGIDKLRGSSYSWVWENRYRREMTLYVDLALFPLVDVRLYPEKVTETL 300
DB 241 DHCVAVYWGIDKLRGSSYSWVWENRYRREMTLYVDLALFPLVDVRLYPEKVTETL 300
QY 301 RDVLTDPVGVNNLRGYGTTFNSNIENYIRKPHLFDYLRHRIOPTRROPQYNDSTNYS 360
DB 301 RDVLTDPVGVNNLRGYGTTFNSNIENYIRKPHLFDYLRHRIOPTRROPQYNDSTNYS 360
QY 361 GNYSTPISGNDITSPYGNKSEPVONLEFNGEKYRAVANTNLAVMPSAVYSGYT 420
DB 361 GNYSTPISGNDITSPYGNKSEPVONLEFNGEKYRAVANTNLAVMPSAVYSGYT 420
QY 421 KVEFSQYNDQTDASTQYTDKRNAGVAMSDSIDOLPPTTDEPLEKYSHQNLVWCF 480
DB 421 KVEFSQYNDQTDASTQYTDKRNAGVAMSDSIDOLPPTTDEPLEKYSHQNLVWCF 480
QY 481 MGSRGITPILWTHKSVDFPNKIDSKITVQLPLVKAYKLOGASVAVAGPRTGGDITOC 540
DB 481 MGSRGITPILWTHKSVDFPNKIDSKITVQLPLVKAYKLOGASVAVAGPRTGGDITOC 540
QY 541 TENGSAATITVTPDVYSQYRARIHYASTQITFTLSLDGAPRNOYTFKTIKGDIT 600
DB 541 TENGSAATITVTPDVYSQYRARIHYASTQITFTLSLDGAPRNOYTFKTIKGDIT 600
QY 601 YNSFNLASFPPELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644
DB 601 YNSFNLASFPPELSGNNLQIGVGLSAGDKVYIDKIEFIPVN 644

```

RESULT 2

```

; Sequence 53, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-943-692-53

```

```

Query Match 3.1%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 33 PNPTELDLVYKEFLRMTADN 52
DB 1 PNPTELDLVYKEFLRMTADN 20

```

RESULT 3

```

; Sequence 3, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.

```

```

; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-943-692-3

```

```

Query Match 2.3%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 4

```

; Sequence 47, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 47
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-943-692-47

```

```

Query Match 1.9%; Score 12; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MNPNNRSEHDTI 12
DB 1 MNPNNRSEHDTI 12

```

RESULT 5

```

; Sequence 50, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: MCPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT APPLICATION NUMBER: US/09/943,692
; PRIOR FILING DATE: 2001-08-31

```

PRIOR APPLICATION NUMBER: 09/027, 998
 PRIOR FILING DATE: 1998-02-23
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 50
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Bacillus thuringiensis
 US-09-943-692-50

Query Match
 Best Local Similarity 100.0%; Score 12; DB 10; Length 12;
 Pred. No. 2.5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 VYDKIEFIPVN 644
 DB 1 VYDKIEFIPVN 12

RESULT 6
 US-09-943-692-26
 Sequence 26, Application US/09943692
 Patent No. US20020152496A1
 GENERAL INFORMATION:
 APPLICANT: FISCHHOFF, DAVID A.
 APPLICANT: FUCHS, ROY L.
 APPLICANT: LAVRIK, PAUL B.
 APPLICANT: MCPHERSON, SYLVIA A.
 APPLICANT: PERILAK, FREDERICK J.
 TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
 FILE REFERENCE: MOBT.195--1
 CURRENT APPLICATION NUMBER: US/09/943,692
 CURRENT FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: 09/027,998
 PRIOR FILING DATE: 1998-02-23
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 26
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Chimeric toxin
 US-09-943-692-26

Query Match
 Best Local Similarity 100.0%; Score 11; DB 10; Length 13;
 Pred. No. 0.00027;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ADNNTALDSS 60
 DB 3 ADNNTALDSS 13

RESULT 7
 US-10-032-717-8
 Sequence 8, Application US/10032717
 Patent No. US20020151709A1
 GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Nicholas B. Duck
 APPLICANT: Xiang Feng
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Theodore W. Kahn
 APPLICANT: Lynn E. Sims
 TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
 TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
 FILE REFERENCE: 35718/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 CURRENT FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 667
 TYPE: PRT
 ORGANISM: Bacillus thuringiensis (truncated)
 US-10-032-717-8

Query Match
 Best Local Similarity 100.0%; Score 10; DB 12; Length 667;
 Pred. No. 0.097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 RREMTLVLD 278
 DB 272 RREMTLVLD 281

RESULT 8
 US-10-032-717-18
 Sequence 18, Application US/10032717
 Patent No. US20020151709A1
 GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Nicholas B. Duck
 APPLICANT: Xiang Feng
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Theodore W. Kahn
 APPLICANT: Lynn E. Sims
 TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
 TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
 FILE REFERENCE: 35718/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 CURRENT FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 18
 LENGTH: 673
 TYPE: PRT
 ORGANISM: Bacillus thuringiensis (truncated)
 US-10-032-717-18

Query Match
 Best Local Similarity 100.0%; Score 10; DB 12; Length 673;
 Pred. No. 0.098;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 RREMTLVLD 278
 DB 272 RREMTLVLD 281

RESULT 9
 US-10-032-717-4
 Sequence 4, Application US/10032717
 Patent No. US20020151709A1
 GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Nicholas B. Duck
 APPLICANT: Xiang Feng
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Theodore W. Kahn
 APPLICANT: Lynn E. Sims
 TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
 TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
 FILE REFERENCE: 35718/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 CURRENT FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 1210

TYPE: PRT
ORGANISM: *Bacillus thuringiensis*
US-10-032-717-4

Query Match
Best Local Similarity 1.6%; Score 10; DB 13; Length 1210;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 272 RREMTLVLD 281

RESULT 10

US-10-120-544A-4
Sequence 4, Application US/10120544A
Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moritichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OPI335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1316
TYPE: PRT
ORGANISM: *Bacillus popilliae*
US-10-120-544A-4

Query Match
Best Local Similarity 1.6%; Score 10; DB 9; Length 1316;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 297 RREMTLVLD 306

RESULT 11

US-10-120-544A-18
Sequence 18, Application US/10120544A
Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moritichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OPI335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463

PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 1332
TYPE: PRT
ORGANISM: *Bacillus popilliae*
US-10-120-544A-18

Query Match
Best Local Similarity 1.6%; Score 10; DB 9; Length 1332;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 257 RREMTLVLD 266

RESULT 12

US-10-120-544A-6
Sequence 6, Application US/10120544A
Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moritichi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OPI335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1386
TYPE: PRT
ORGANISM: *Bacillus popilliae*
US-10-120-544A-6

Query Match
Best Local Similarity 1.6%; Score 10; DB 9; Length 1386;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLD 278
DB 298 RREMTLVLD 307

RESULT 13
US-09-738-363-31
Sequence 31, Application US/09738363
Patent No. US20010010932A1
GENERAL INFORMATION:
APPLICANT: Schepf, Harry E.
Schwab, George E.
Payne, Jewel M.
Narva, Kenneth E.
Foncerrada, Luis

TITLE OF INVENTION: Nematocidal Proteins
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville

STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-738-363-31

Query Match 1.4%; Score 9; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 634 YIDKIEFIP 642
|||||

DB 1 YIDKIEFIP 9

RESULT 14
US-09-943-692-29
Sequence 29, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAVRIK, PAUL B.
APPLICANT: McPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195--1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-29

Query Match 1.2%; Score 8; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 77 LGVVGPF 84
|||||

DB 2 LGVVGPF 9

RESULT 15
US-09-943-692-20
Sequence 20, Application US/09943692
Patent No. US20020152496A1
GENERAL INFORMATION:
APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FUCHS, ROY L.
APPLICANT: LAVRIK, PAUL B.
APPLICANT: McPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBT:195--1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/027,998
PRIOR FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-20

Query Match 1.2%; Score 8; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 633 YIDKIEF 640
|||||

DB 1 YIDKIEF 8

Search completed: January 10, 2003, 11:11:43
Job time : 12 secs

1.
2.

1.
2.

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:08:29 ; Search time 21 Seconds
(without alignments)
2948.122 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MPNNRSEHDTKTENNENY.....TGLSNGDKVYIDKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR_73.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	652	2 A27323	parasporal crystal
2	23	3.6	649	1 JH0261	parasporal crystal
3	21	3.3	652	2 I39811	parasporal crystal
4	21	3.3	659	2 S10228	parasporal crystal
5	11	1.7	934	2 B28838	parasporal crystal
6	9	1.4	1157	1 S49247	parasporal crystal
7	8	1.2	260	2 A70248	hypothetical prote
8	8	1.2	329	2 D97340	DNA replication pr
9	8	1.2	357	2 AC2045	6-phosphofructokin
10	8	1.2	375	2 E75542	probable endogluc
11	8	1.2	483	2 T36811	probable integral
12	8	1.2	760	2 T24521	hypothetical prote
13	8	1.2	1138	2 A48944	parasporal crystal
14	8	1.2	1154	2 S39536	parasporal crystal
15	8	1.2	1156	2 S19306	parasporal crystal
16	8	1.1	57	2 H90881	hypothetical prote
17	7	1.1	57	2 A85737	hypothetical prote
18	7	1.1	89	2 A11499	hypothetical prote
19	7	1.1	130	2 T14749	hypothetical prote
20	7	1.1	133	2 T47132	translation initia
21	7	1.1	135	2 B69103	hypothetical prote
22	7	1.1	140	2 AC1280	hypothetical prote
23	7	1.1	140	2 AC1643	hypothetical prote
24	7	1.1	143	2 S23255	TSC-22 protein - m
25	7	1.1	144	2 JC4813	TGF beta-stimulate
26	7	1.1	162	2 T36328	probable secreted
27	7	1.1	162	2 AH0480	probable membrane
28	7	1.1	197	2 C70519	hypothetical prote
29	7	1.1	217	2 G84045	transcription regu

30	7	1.1	224	2 C82973	hypothetical prote
31	7	1.1	225	2 F87528	hypothetical prote
32	7	1.1	227	2 F70529	probable trka prot
33	7	1.1	227	2 G69491	conserved hypothet
34	7	1.1	230	2 T06309	glutathione peroxi
35	7	1.1	233	2 A69004	cpdacylglycerol-
36	7	1.1	233	2 C75290	hypothetical prote
37	7	1.1	243	2 C86758	hypothetical prote
38	7	1.1	259	2 E84125	hydroxylase BH3805
39	7	1.1	261	2 S53090	CD40 ligand - bov
40	7	1.1	265	2 J00435	arcelin-2 - kidney
41	7	1.1	265	2 A40111	arcelin-1 seed pro
42	7	1.1	265	2 A95971	probable sugar apt
43	7	1.1	275	2 A95971	amino acid ABC tra
44	7	1.1	277	2 G71849	glutamine ABC tran
45	7	1.1	288	2 AE3632	galactoside transp

ALIGNMENTS

RESULT 1

A27323 parasporal crystal protein crystal - Bacillus thuringiensis

N:Alternate names: coleopteran-specific insect control protein; crystal protein cryc;

C:Species: Bacillus thuringiensis

C:Date: 19-Nov-1988 #sequence revision 19-Nov-1988 #extLchange 01-Dec-2000

C:Accession: A27323; A26853; A29987; A28407; S60781; I39813

C:Herrnstadt, C.; Gilroy, T.E.; Sobleski, D.A.; Bennett, B.D.; Gaertner, F.H.

Gene 57, 37-46, 1987

A:Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active

A:Reference number: A27323; MUID:88112860; PMID:2828180

A:Accession: A27323

A:Molecule type: DNA

A:Residues: 1-652 <HER>

A:Cross-references: GB:M22472; NID:9142733; PIDN:AAA22336.1; PID:9142734

A:Experimental source: strain San Diego

R:Hoeltje, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.

Nucleic Acids Res. 15, 7183, 1987

A:Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus t

A:Reference number: A26853; MUID:88015559; PMID:3658680

A:Accession: A26853

A:Molecule type: DNA

A:Residues: 9-652 <HOB>

A:Cross-references: GB:Y00420; NID:940252; PIDN:CAA68482.1; PID:940253

A:Experimental source: var. tenebrionis

R:McPherson, S.A.; Perlek, F.J.; Fuchs, R.L.; Marone, P.G.; Lavrik, P.B.; Fischhoff,

Bio/Technology 6, 61-66, 1988

A:Title: Characterization of the coleopteran-specific protein gene of Bacillus thurin

A:Reference number: A29987

A:Accession: A29987

A:Molecule type: DNA

A:Residues: 9-652 <SEK>

A:Experimental source: var. tenebrionis

R:Adams, L.F.; Mathews, S.; O'Hara, P.; Petersen, A.; Guertler, H.

Mol. Microbiol. 14, 381-389, 1994

A:Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized stra

A:Reference number: S60781; MUID:95131759; PMID:7830581

A:Accession: S60781

A:Molecule type: DNA

A:Residues: 9-652 <ADA>

A:Cross-references: EMBL:U10985; NID:9506182; PIDN:AAC43266.1; PID:9514312

A:Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

R.Wu, S.J.; Dean, D.H.
 J. Mol. Biol. 255, 628-640, 1996
 A:Title: Functional significance of loops in the receptor binding domain of Bacillus thuringiensis
 A:Reference number: S62317; MUID:96163559; PMID:8568902
 A:Contents: annotation
 R:Donovan, W.P.; Gonzalez, J.M.
 Mol. Gen. Genet. 214, 365-372, 1988
 A:Title: Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis
 A:Reference number: I39812; MUID:89112139; PMID:1146015
 A:Accession: I39812
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 9-652 <RES>
 A:Cross-references: GB:M37207; MUID:9142735; PIDN:AAA50255.1; PID:g142736
 A:Experimental source: strain EG2158
 J:Telcelira De Souza, M.; Lecadet, M.M.; Lereclus, D.
 J. Bacteriol. 175, 2952-2960, 1993
 A:Title: Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a
 A:Reference number: I39813; MUID:9355939; PMID:8491716
 A:Accession: I39813
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 9-58 <RE2>
 A:Cross-references: GB:L03393; MUID:9304150; PIDN:AAA22350.1; PID:g551698
 A:Gene: cryIIIA
 C:Genetics:
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 100.0%; Score 644; DB 2; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNPNRSEHDTKTENNEVPINHOVPLAETPPTLEDLNKKFELMTADNNTALDSS 60
 DB 9 MNPNRSEHDTKTENNEVPINHOVPLAETPPTLEDLNKKFELMTADNNTALDSS 68
 61 TTKDVIQGISVVDLGVGPFPGALVSRYTNFLMTINPSDEPMKAEQVEALMDOK 120
 DB 69 TTKDVIQGISVVDLGVGPFPGALVSRYTNFLMTINPSDEPMKAEQVEALMDOK 128
 121 IADYAKNALAELOGLQNNVEDVYSAISWQKNPVSSRNPHSGQRIREFSQASHFRNS 180
 DB 129 IADYAKNALAELOGLQNNVEDVYSAISWQKNPVSSRNPHSGQRIREFSQASHFRNS 188
 181 MPSPAIISGEVLFITTYAQAANTHLFLKDAQITGEEMGEKEDIAPFYKROKLTQERT 240
 DB 189 MPSPAIISGEVLFITTYAQAANTHLFLKDAQITGEEMGEKEDIAPFYKROKLTQERT 248
 241 DHCKKYNVGLDKLRGSSYSSEWVFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 300
 DB 249 DHCKKYNVGLDKLRGSSYSSEWVFNRYRREMTLVLDLALFPLVDVRLYPREVTELT 308
 301 RDVLTDPVGVNLRGCTFESNENYIRKPHLEFDYLRHQFTRRQPGTYGNDSEFNWS 360
 DB 309 RDVLTDPVGVNLRGCTFESNENYIRKPHLEFDYLRHQFTRRQPGTYGNDSEFNWS 368
 361 GNYVSTSPISGNDITSPFYGNKSEPVONLEFNGEKYRAVANTNLVWPSAVYSGYT 420
 DB 369 GNYVSTSPISGNDITSPFYGNKSEPVONLEFNGEKYRAVANTNLVWPSAVYSGYT 428
 421 KVEFSQVNDOTDEASTQTYDSKRNVGAVSWDSIDOLPEPTTDEPLEKYSQOLNVKCF 480
 DB 429 KVEFSQVNDOTDEASTQTYDSKRNVGAVSWDSIDOLPEPTTDEPLEKYSQOLNVKCF 488
 481 MGSRGCTIPVLTWTHKSVFNNMIDSKITQPLVKAAYLQSGAVVAGPRRTGDDITQC 540
 DB 489 MGSRGCTIPVLTWTHKSVFNNMIDSKITQPLVKAAYLQSGAVVAGPRRTGDDITQC 548
 541 TENGSAATYVPPDVYSQKTYARHIVASTSQITFTLSLDGAPFNQYFEDTKNGDTLT 600
 DB 549 TENGSAATYVPPDVYSQKTYARHIVASTSQITFTLSLDGAPFNQYFEDTKNGDTLT 608

QY 601 YNSFNLSFSTPELSEGNITQIGVTLGSLGDKYIDKIEFIQVN 644
 DB 609 YNSFNLSFSTPELSEGNITQIGVTLGSLGDKYIDKIEFIQVN 652

RESULT 2

JH0261
 parasporal crystal protein cry3cal - Bacillus thuringiensis subsp. kurstaki (strain B
 N:Alternate names: parasporal crystal protein cryIIID
 C:Species: Bacillus thuringiensis subsp. kurstaki
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 01-Dec-2000
 A:Accession: JH0261; S18944
 R:Lambert, B.; Theunis, W.; Ayuda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Se
 Gene 110, 131-132, 1992
 A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crys
 A:Reference number: JH0261; MUID:92184108; PMID:1544571
 A:Accession: JH0261
 A:Molecule type: DNA
 A:Residues: 1-649 <LAM>
 A:Cross-references: EMBL:X59797; MUID:940287; PIDN:CAA42469.1; PID:g40288
 C:Genetics:
 A:Gene: cryIIID
 C:Superfamily: parasporal crystal protein

Query Match 3.6%; Score 23; DB 1; Length 649;
 Best Local Similarity 100.0%; Pred. No. 2,6e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 GYGTFESNENYIRKPHLEFDYLH 338
 DB 314 GYGTFESNENYIRKPHLEFDYLH 336

RESULT 3

I39811
 N:Alternate names: parasporal crystal protein cryIIIB2
 C:Species: Bacillus thuringiensis
 C:Date: 19-Jul-1996 #sequence-revision 19-Jul-1996 #text-change 01-Dec-2000
 A:Accession: I39811
 R:Donovan, W.P.; Ruper, M.T.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson,
 Appl. Environ. Microbiol. 58, 3921-3927, 1992
 A:Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal c
 A:Reference number: I39811; MUID:93119147; PMID:1476436
 A:Accession: I39811
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-652 <RES>
 A:Cross-references: GB:M89794; MUID:9142729; PIDN:AAA22334.1; PID:g142730
 C:Genetics:
 A:Gene: cryIIIB2
 C:Superfamily: parasporal crystal protein

Query Match 3.3%; Score 21; DB 2; Length 652;
 Best Local Similarity 100.0%; Pred. No. 3.3e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 RIRELFSQASHFRNMPSPA 185
 DB 166 RIRELFSQASHFRNMPSPA 186

RESULT 4

S10228
 parasporal crystal protein cry3bal - Bacillus thuringiensis (fragment)
 N:Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
 C:Species: Bacillus thuringiensis
 C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 01-Dec-2000
 A:Accession: S10228
 R:Stick, A.; Gaertner, F.; Wong, A.
 Nucleic Acids Res. 18, 1305, 1990
 A:Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of
 A:Reference number: S10228; MUID:90206811; PMID:2320431

A:Accession: S10228
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-659 <SIC>
 A:Cross-references: EMBL:X17123; NID:940258; PIDN:CAA34983.1; PID:940255
 C:Genetics:
 A:Gene: cryIIIB
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin; toxin

Query Match 3.3%; Score 21; DB 2; Length 659;
 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 RIRLFQASHFRNMPSTRA 185
 |||||
 DB 174 RIRLFQASHFRNMPSTRA 194

RESULT 5
 B29838
 parasporal crystal protein - *Bacillus thuringiensis* subsp. *israelensis* (fragment)
 C:Species: *Bacillus thuringiensis* subsp. *israelensis*
 C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 01-Dec-2000
 C:Accession: B29838
 R:Rhone, L.; Garduno, F.; Thompson, T.; Decker, D.; Zouner, M.; Wild, M.; Walfield, A.M.
 J. *Bacteriol.* 166, 801-811, 1986
 A:Title: Structural similarity between the lepidoptera- and diptera-specific insecticide
 A:Reference number: A94672; MUID:86223796; PMID:3011746
 A:Accession: B29838
 A:Molecule type: DNA
 A:Residues: 1-934 <TRHO>
 A:Cross-references: GB:M12662; NID:q143228
 C:Superfamily: parasporal crystal protein

Query Match 1.7%; Score 11; DB 2; Length 934;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 271 EMTLVLDLIA 281
 |||||
 DB 284 EMTLVLDLIA 294

RESULT 6
 S49247
 parasporal crystal protein cry9ca1 [validated] - *Bacillus thuringiensis*
 N:Alternate names: parasporal crystal protein cryIH
 C:Species: *Bacillus thuringiensis*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 C:Accession: A59350; S49247
 R:Limbert, B.; Buyse, L.; Decock, C.; Janssens, S.; Plans, C.; Saey, B.; Seurlinck, J.; V.
 Appl. Environ. Microbiol. 62, 860-86, 1996
 A:Title: A *Bacillus thuringiensis* insecticidal crystal protein with a high activity against
 A:Reference number: A59350; MUID:96141404; PMID:8572715
 A:Accession: A59350
 A:Molecule type: DNA
 A:Residues: 1-1157 <LAM>
 A:Cross-references: EMBL:Z37527; NID:9547554; PIDN:CAA85764.1; PID:9547556
 A:Experimental source: serovar toluworth
 C:Comment: This parasporal crystal protein, active against corn borer and other insects,
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 1.4%; Score 9; DB 1; Length 1157;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 ITOLPLVKA 517
 |||||
 DB 515 ITOLPLVKA 523

RESULT 7
 A70248
 hypothetical protein BBJ24 - Lyme disease spirochete plasmid J/1p38
 C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
 C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
 C:Accession: A70248
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh.
 son, D.; Peterson, J.; Kervatage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yu
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A:Reference number: A70100; MUID:9805943; PMID:9403685
 A:Accession: A70248
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-260 <KLE>
 A:Cross-references: GB:AE000787; NID:92690175; PIDN:AA66120.1; PID:92690212; TIGR:BB
 A:Experimental source: strain B31
 C:Genetics:
 A:Genome: plasmid

Query Match 1.2%; Score 8; DB 2; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 632 KYIDKIE 639
 |||||
 DB 22 KYIDKIE 29

RESULT 8
 D97340
 DNA replication protein DnaC [imported] - *Clostridium acetobutylicum*
 C:Species: *Clostridium acetobutylicum*
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: D97340
 R:Rolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. *Bacteriol.* 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing *Bacterium*
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97340
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-329 <KUN>
 A:Cross-references: GB:AE001437; PIDN:NAK81511.1; PID:q15026685; GSPDB:GN00168
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC3588

Query Match 1.2%; Score 8; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 PNPTLEDL 40
 |||||
 DB 235 PNPTLEDL 242

RESULT 9
 AC2045
 6-phosphofructokinase [imported] - *Nostoc* sp. (strain PCC 7120)
 C:Species: *Nostoc* sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AC2045
 R:Kaneh, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriju
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC2045

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA073612.1; PID:q17131003; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alt1913
 C:Superfamily: 6-phosphofructokinase; 6-phosphofructokinase 1 homology

Query Match 1.2%; Score 8; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 592 TINKGDTL 599
 |||||||
 DB 77 TINKGDTL 84

RESULT 10
 E75542
 Probable endoglucanase - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: E75542
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 246, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75542
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-375 <KMT>
 A:Cross-references: GB:AE00186; GB:AE000513; NID:g6457921; PIDN:AAF09817.1; PID:g645790
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0229
 A:Map position: 1
 C:Superfamily: thermophilic aminopeptidase I alpha chain

Query Match 1.2%; Score 8; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GDLGTVG 81
 |||||||
 DB 132 GDLGTVG 139

RESULT 11
 T36811

probable integral membrane transport protein - *Streptomyces coelicolor*
 C:Species: *Streptomyces coelicolor*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36811
 R:Olliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rejandream, M.A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21614
 A:Accession: T36811
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <OLIT>
 A:Cross-references: EMBL:AL096811; PIDN:CA046808.1; GSPDB:GN00070; SCODEB:SCI30A.31C
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCODEB:SCI30A.31C

Query Match 1.2%; Score 8; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 576 TSLSDGAP 583

DB 205 TSLSDGAP 212
 |||||||

RESULT 12
 T24521

hypothetical protein T05E11.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T24521
 R:Kershaw, J.

submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19903
 A:Accession: T24521
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-760 <WIL>
 A:Cross-references: EMBL:Z68751; PIDN:CA092973.1; GSPDB:GN00022; CESP:T05E11.3
 A:Experimental source: clone T05E11
 C:Genetics:
 A:Gene: CESP:T05E11.3
 A:Map position: 4
 A:Insertions: 16/1; 39/2; 378/3; 570/3
 C:Superfamily: heat shock protein 90

Query Match 1.2%; Score 8; DB 2; Length 760;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 188 GYEVLEFLT 195
 |||||||
 DB 539 GYEVLEFLT 546

RESULT 13
 A48944

parasporal crystal protein cry7mal - *Bacillus thuringiensis*
 N:Alternate names: parasporal crystal protein cryIIIC
 C:Species: *Bacillus thuringiensis*
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
 C:Accession: A48944
 R:Lambert, B.; Holte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.

Appl. Environ. Microbiol. 58, 2536-2542, 1992
 A:Title: Novel *Bacillus thuringiensis* insecticidal crystal protein with a silent acti
 A:Reference number: A48944; MUID:92384571; PMID:1514800
 A:Contents: B7S1377
 A:Accession: A48944
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-1138 <LAM>
 A:Cross-references: GB:M64478; NID:g142760; PIDN:AAA22351.1; PID:g142761
 A:Note: sequence extracted from NCBI backbone (NCBI:n112092, NCBI:n112093)
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 1.2%; Score 8; DB 2; Length 1138;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 451 DSIQDLPP 458
 |||||||
 DB 438 DSIQDLPP 445

RESULT 14
 S39536

parasporal crystal protein cry9bal - *Bacillus thuringiensis*
 N:Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
 C:Species: *Bacillus thuringiensis*
 C:Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
 C:Accession: S39536
 R:Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Ste
 FEBS Lett. 336, 79-82, 1993

A:Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bacillus thuringiensis
 A:Reference number: S39536; MUID:94085596; PMID:8262221
 A:Accession: S39536
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1154 <SHE>
 A:Cross-references: EMBL:X75019
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 1.2%; Score 8; DB 2; Length 1154;
 Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 ITQPLVVK 516
 |||||
 DB 517 ITQPLVVK 524

RESULT 15

S19306

parasporal crystal protein cry9Aa1 - Bacillus thuringiensis

N:Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal protein

C:Species: Bacillus thuringiensis

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000

C:Accession: S19306; S23588; A44847; S14602; S14837

R:Smulevitch, S.V.; Osterman, A.L.; Shevelov, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrc

FEBS Lett. 293, 25-28, 1991

A:Title: Nucleotide sequence of a novel delta-endotoxin gene cryIc of Bacillus thuringiensis

A:Reference number: S19306; MUID:92070568; PMID:1660003

A:Accession: S19306

A:Molecule type: DNA

A:Residues: 1-1156 <SMU>

A:Cross-references: EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:940271

A:Experimental source: subsp. galleriae

A:Accession: S23588

A:Molecule type: protein

A:Residues: 24-34 <SMU1>

A:Experimental source: subsp. galleriae

R:Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.

J. gen. Microbiol. 138, 55-62, 1992

A:Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis

A:Reference number: A44847; MUID:92211329; PMID:156556

A:Accession: A44847

A:Molecule type: DNA

A>Status: preliminary

A:Cross-references: EMBL:X58534; NID:948879; PIDN:CAA41425.1; PID:948880

A:Experimental source: isolate DSIR517

A:Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBI:92867)

C:Genetics:

A:Gene: cryIG

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 1.2%; Score 8; DB 2; Length 1156;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 RYRREMTL 274
 |||||
 DB 267 RYRREMTL 274

Search completed: January 10, 2003, 11:11:04
 Job time : 24 secs

100

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:07:39 ; Search time 14 Seconds
(without alignments)
1907.911 Million cell updates/sec

Title: US-09-943-692-2

Perfect score: 644
Sequence: 1 MNPNNRSEHDTIKTENNEV.....TGLSAGDKVYIDKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	644	1	C3AA_BACTT
2	23	3.6	649	1	C3CA_BACTK
3	21	3.3	652	1	C3BB_BACTU
4	21	3.3	659	1	C3BA_BACTO
5	17	2.6	648	1	C3AA_BACTJ
6	11	1.7	675	1	C3AA_BACTI
7	11	1.7	675	1	C3AA_BACTJ
8	10	1.6	682	1	C3BA_BACTH
9	10	1.6	1169	1	C8BA_BACTK
10	10	1.6	1169	1	C9DA_BACTP
11	9	1.4	674	1	C9AA_BACTO
12	9	1.4	826	1	C9AA_BACTO
13	9	1.4	1157	1	C9CA_BACTO
14	8	1.2	618	1	C9AA_CLOBI
15	8	1.2	1138	1	C7AB_BACTU
16	8	1.2	1138	1	C7AB_BACTU
17	8	1.2	1138	1	C7AB_BACTU
18	8	1.2	1156	1	C9AA_BACTG
19	7	1.1	82	1	ATPH_OCHNE
20	7	1.1	134	1	ATPH_OCHNE
21	7	1.1	134	1	ATPH_OCHNE
22	7	1.1	135	1	ATPH_OCHNE
23	7	1.1	135	1	ATPH_OCHNE
24	7	1.1	143	1	ATPH_OCHNE
25	7	1.1	143	1	ATPH_OCHNE
26	7	1.1	157	1	ATPH_OCHNE
27	7	1.1	157	1	ATPH_OCHNE
28	7	1.1	201	1	ATPH_OCHNE
29	7	1.1	261	1	ATPH_OCHNE
30	7	1.1	265	1	ATPH_OCHNE
31	7	1.1	265	1	ATPH_OCHNE
32	7	1.1	327	1	ATPH_OCHNE
33	7	1.1	327	1	ATPH_OCHNE

ALIGNMENTS

RESULT 1	ID	C3AA_BACTT	STANDARD:	PRT:	644 AA.
AC	P07130	P21255			
DT	01-APR-1988	(Rel. 07, Created)			
DT	01-APR-1988	(Rel. 07, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Pesticidal crystal protein cry3Aa precursor (insecticidal delta-endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa crystal protein).				
GN	CRY3AA OR CRYIIIA(A) OR CRYIIA OR CRY3A OR CRYC OR B13.				
OS	Bacillus thuringiensis (subsp. tenebrionis), and				
OS	Bacillus thuringiensis (subsp. morrisoni), and				
OS	Bacillus thuringiensis (subsp. san diego).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1444, 1441, 1435;				
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis;				
RX	MEDLINE=88015559; PubMed=3658680;				
RA	Hoefte H., Seurinck J., Houtven A.V., Vaack M.;				
RT	"Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";				
RL	Nucleic Acids Res. 15:7183-7183(1987).				
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis;				
RX	McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavyk P.B.,				
RA	Fischhoff D.A.;				
RT	"Characterization of the coleopteran-specific protein gene of Bacillus thuringiensis var. tenebrionis.";				
RL	Biotechnology 6:61-66(1988).				
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis; STRAIN=NB176;				
RX	MEDLINE=95131759; PubMed=7830581;				
RA	Adams L.F., Mathews S., O'Hara P., Petersen A., Guttler H.;				
RT	"Elucidation of the mechanism of CryIIIA overproduction in a mutantized strain of Bacillus thuringiensis var. tenebrionis.";				
RL	Mol. Microbiol. 14:381-389(1994).				
RN					
RP	SEQUENCE FROM N.A.				
RC	SPECIES-B.t.tenebrionis; STRAIN=EG2158;				
RX	MEDLINE=89112139; PubMed=3146015;				
RA	Donovan W.P., Gonzalez J.M. Jr., Gilbert M.P., Dankocsik C.C.;				
RT	"Isolation and characterization of EG2158, a new strain of Bacillus thuringiensis toxic to coleopteran larvae, and nucleotide sequence of the toxin gene.";				
RL	Mol. Gen. Genet. 214:365-372(1988).				

34	7	1.1	330	1	YETK_BACSU	021540 bacillus su
35	7	1.1	366	1	CHAA_ECOLI	P31801 escherichia
36	7	1.1	388	1	SUCC_PASMU	09cnd0 pasteurella
37	7	1.1	390	1	PRGC_SULSO	09ux05 sulfolobus
38	7	1.1	411	1	Y360_MYCGE	049426 mycoplasma
39	7	1.1	411	1	PHAL_PSELE	P52090 pseudomonas
40	7	1.1	428	1	DCDA_METHH	027390 methanobact
41	7	1.1	444	1	YMDA_BACSU	P39584 bacillus su
42	7	1.1	474	1	IRX2_MOUSE	P81066 mus musculu
43	7	1.1	530	1	UD18_RAT	064634 rattus norv
44	7	1.1	562	1	AMAL_PLAFR	P22622 plasmodium
45	7	1.1	563	1	PK66_PLAKU	P21303 plasmodium

```

RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES-B.t.san diego;
RX MEDLINE-88112860; Pubmed-2828180;
RA Herrnstadt C., Gilroy T.E., Sobleski D.A., Bennett B.D.,
RA Geertner F.H.;
RT "Nucleotide sequence and deduced amino acid sequence of a coleopteran-
RT active delta-endotoxin gene from Bacillus thuringiensis subsp. san
RT diego.";
RL Gene 57:37-46(1987).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC SPECIES-B.t.tenebrionis;
RX MEDLINE-92049729; Pubmed-1658659;
RA Li J., Carroll J., Ellar D.J.;
RT Crystal structure of insecticidal delta-endotoxin from Bacillus
RT thuringiensis at 2.5-A resolution.";
RL Nature 353:815-821(1991).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
CC insect-resistant potato by Monsanto.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y00420; CAA68482.1; -
DR EMBL: J02978; AAA22541.1; -
DR EMBL: M37207; AAA50255.1; -
DR EMBL: U10985; AAC43266.1; -
DR EMBL: M30503; AAA22542.1; -
DR EMBL: M2472; AAA22336.1; ALT_INT.
DR PIR: A26853; A26853.
DR PIR: A28407; A28407.
DR PIR: A29987; A29987.
DR PIR: A27323; A27323.
DR PDB: 1DLC; 30-SEP-94.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation; 3D-structure; Genetically modified food.
FT PROPEP 1 57 REMOVED IN MATURE FORM.
FT CHAIN 58 644 PESTICIDIAL CRYSTAL PROTEIN CRY3AA.
FT CONFLICT 544 544 G -> A (IN REF. 3).
SO SEQUENCE 644 AA; 73108 MW; EFCEFLCEFD9683 CRC64;
Query Match 100.0%; Score 644; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

DB 181 MPSPALSGYEVLFITTYAQAANTHFLKDAQITGCEMCEYKEDIAEFYKRLKLTQET 240
QY DHCKYKYNVGLDKRGSSYSWVNFNRYRREMTLYLDIALFPYLDVRLYKEVKTELT 300
DB 241 DHCKYKYNVGLDKRGSSYSWVNFNRYRREMTLYLDIALFPYLDVRLYKEVKTELT 300
QY 301 RDVLTDPVGVNMLRGYGTFSNIENYIRKPHLFDVLRHQPFHFGYGYGNSFNYS 360
DB 301 RDVLTDPVGVNMLRGYGTFSNIENYIRKPHLFDVLRHQPFHFGYGYGNSFNYS 360
QY 361 GNVYSPRPSIGSNDITSPYGNKSEPOVNEFNGEKYRAVANTNLAVPSAYSGVT 420
DB 361 GNVYSPRPSIGSNDITSPYGNKSEPOVNEFNGEKYRAVANTNLAVPSAYSGVT 420
QY 421 KVEFSQYNDQDEASQYDYSKRNKAVSMDSIDLPETDEPELEKYSQOLVYKEL 480
DB 421 KVEFSQYNDQDEASQYDYSKRNKAVSMDSIDLPETDEPELEKYSQOLVYKEL 480
QY 481 MOGSRGTIPVLTWTKRSVDFENKIDSKITQPLVYKAYKLGASVAGPFTGDIIC 540
DB 481 MOGSRGTIPVLTWTKRSVDFENKIDSKITQPLVYKAYKLGASVAGPFTGDIIC 540
QY 541 TENGSAATITVPDYSQYKARIVASTQIPTLSLDGAPRQYFEKTIKGDIT 600
DB 541 TENGSAATITVPDYSQYKARIVASTQIPTLSLDGAPRQYFEKTIKGDIT 600
QY 601 YNSFNLASFTPELGSNNLQIGVTLSAGDKVYIDKIEFIPN 644
DB 601 YNSFNLASFTPELGSNNLQIGVTLSAGDKVYIDKIEFIPN 644
RESULT 2
C3CA_BACTK STANDARD; PRT; 649 AA.
ID C3CA_BACTK
AC 045744;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidial crystal protein cry3ca (insecticidal delta-endotoxin
DE CryIIIC(a)) (Crystalline entomocidal protoxin) (73 kDa crystal
DE protein).
GN CRY3CA OR CRYIIIC(A) OR CRYIIID.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN-BT1109P;
RA MEDLINE-92184108; Pubmed-1544571;
RA Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C.,
RA Jansens S., Seurinck J., Peferoen M.;
RT "Nucleotide sequence of gene cryIIID encoding a novel coleopteran-
RT active crystal protein from strain BT1109P of Bacillus thuringiensis
RT subsp. kurstaki.";
RL Gene 110:131-132(1992).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----

```


RESULT 5
CJAA_BACTU STANDARD: PRT: 648 AA.
AC 032307;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry19aA (insecticidal delta-endotoxin
DE CRY19A(a)) (Crystalline entomocidal protoxin) (75 kDa crystal
protein).
GN CRY19AA OR CRY19A(A).
OS Bacillus thuringiensis (subsp. jegathesan).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=56955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=367;
RX MEDLINE=98027382; PubMed=9361431;
RA Rosso M.L., Delecluse A.;
RT "Contribution of the 65-kilodalton protein encoded by the cloned gene
RT cry19a to the mosquitoicidal activity of Bacillus thuringiensis subsp.
RT jegathesan.";
RL Appl. Environ. Microbiol. 63:4449-4455(1997).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MOSQUITOS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE MATURATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y07603; CAA68875.1; -.
DR HSP: P07130; IDIC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 648 AA; 74742 MW; E4A8FBA4570DE5B9 CRC64;
Query Match 2.6%; Score 17; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 262 WNFENRVRREMTLVLD 278
DB 267 WNFENRVRREMTLVLD 283
RESULT 6
CAAA_BACTU STANDARD: PRT: 675 AA.
AC P09662;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry10aA (insecticidal delta-endotoxin
DE CRY10A(a)) (Crystalline entomocidal protoxin) (78 kDa crystal
protein).
GN CRY10AA OR CRY10(A) OR CRY10C.
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=ONR60A;
RX MEDLINE=86223796; PubMed=3011746;
RA Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M.,
RA Wallfield A.M., Pollock T.J.;
RT "Structural similarity between the lepidoptera- and diptera-specific
RT insecticidal endotoxin genes of Bacillus thuringiensis subsp.
RT 'kurstaki' and 'israelensis'";
RL J. Bacteriol. 166:801-811(1986).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MOSQUITOS. ACTIVE ON AEGES AEGYPT.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE MATURATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M12662; AAA22614.1; -.
DR PIR: B29838; B29838.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 675 AA; 77760 MW; 2A70011BEA7985F5 CRC64;
Query Match 1.7%; Score 11; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 271 EMTLVLDLIA 281
DB 284 EMTLVLDLIA 294
RESULT 7
CPAA_BACTU STANDARD: PRT: 675 AA.
AC O87906;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry25aA (insecticidal delta-endotoxin
DE CRY25A(a)) (Crystalline entomocidal protoxin) (76 kDa crystal
protein).
GN CRY25AA OR CRY25A(A).
OS Bacillus thuringiensis (subsp. jegathesan).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=56955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawalek M.D., Gill S.S.;
RT "Isolation and characterization of insecticidal genes from Bacillus
RT thuringiensis subsp. jegathesan.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE MATURATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: U88189; AAC61892.1; -
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 675 AA; 75642 MW; 509CC9F1F7501459 CRC64;

Query Match 1.7%; Score 11; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLDL 279
DB 277 RREMTLVLDL 287

RESULT 8

ID CUBA_BACUH STANDARD; PRT; 682 AA.

AC 086170;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry19Ba (insecticidal delta-endotoxin
DE CRY19Ba(a)) (Crystalline entomocidal protoxin) (78 kDa crystal
DE protein).
GN CRY19Ba OR CRY19Ba(A).
OS Bacillus thuringiensis (subsp. hl90).
OC Plasmid.
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132266;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98369730; PubMed-9704107;
RA Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Ohba M.;
RT "A novel class of mosquitocidal delta-endotoxin, Cry19B, encoded by a
RT Bacillus thuringiensis serovar hl90 gene.";
RL Syst. Appl. Microbiol. 21:179-184(1998).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MOSQUITOS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: D88381; AAA32397.1; -
DR HSSP: P07130; IDIC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation; Plasmid.
SQ SEQUENCE 682 AA; 78490 MW; 5351EA63E2B042F7 CRC64;

Query Match 1.6%; Score 10; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 265 FNRRTREMTL 274
DB 258 FNRRTREMTL 267

RESULT 9

ID C8BA_BACUK STANDARD; PRT; 1169 AA.

AC 045705;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry8Ba (insecticidal delta-endotoxin
DE CRY8Ba(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
DE protein).
GN CRY8Ba OR CRY8Ba(A) OR 50C(B).
OS Bacillus thuringiensis (subsp. kumamotoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NRRL B-18746 / PS50C;
RA Michaels T.E., Fencera L., Narva K.E.;
RT "Process for controlling scarab pests with Bacillus thuringiensis
RT isolates.";
RL Patent number WO9315206, 05-AUG-1993.

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABEID BEETLES.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: U04365; AAA21118.1; -
DR HSSP: P07130; IDIC.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1169 AA; 133543 MW; 22EEFCE5BD699909 CRC64;

Query Match 1.6%; Score 10; DB 1; Length 1169;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 RREMTLVLDL 278
DB 272 RREMTLVLDL 281

RESULT 10

ID C9DA_BACTP STANDARD; PRT; 1169 AA.

AC 006014;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry9Da (insecticidal delta-endotoxin
DE CRY9Da(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
DE protein).
GN CRY9Da OR CRY9Da(A).
OS Bacillus thuringiensis (subsp. japonensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=128936;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-N141;

RA Asano S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; D85560; BAA1948.1; -
 DR HSSP; P07130; IDLC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1169 AA; 659AB257229DE5E9 CRC64;
 Query Match 1.6%; Score 10; DB 1; Length 1169;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 509 ITQLPYKAY 518
 Db 531 ITQLPYKAY 540
 RESULT 11
 ID COA_BACTJ STANDARD; PRT; 674 AA.
 AC 087905;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry24Aa (insecticidal delta-endotoxin
 DE CryxIVa(a)) (crystalline entomocidal protoxin) (Crystal protein)
 DE (insecticidal protein Jegg72) (Fragment).
 GN CRY24AA OR CRYXXIVA(A).
 OS Bacillus thuringiensis (subsp. jegathesan).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=56955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawalek M.D., Gill S.S.;
 RT "Isolation and characterization of insecticidal genes from Bacillus
 RT thuringiensis subsp. jegathesan";
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U08188; AAC61891.1; -

DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 FT NON-TER 674 674
 SQ SEQUENCE 674 AA; 75959 MW; DA3904DAB891C978 CRC64;
 Query Match 1.4%; Score 9; DB 1; Length 674;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 635 IDKIEFIPV 643
 Db 640 IDKIEFIPV 648
 RESULT 12
 ID CRAA_BACUH STANDARD; PRT; 826 AA.
 AC 095597;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry27Aa (insecticidal delta-endotoxin
 DE CryxxVIIa(a)) (crystalline entomocidal protoxin) (94 kDa crystal
 DE protein).
 GN CRY27AA OR CRYXXVIIA(A).
 OS Bacillus thuringiensis (subsp. higo).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=132266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saitoh H.;
 RT "94kDa mosquitocidal toxin from serovar higo";
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB023293; BAA82796.1; -
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 826 AA; 94434 MW; DFD5313C5B6023E2 CRC64;
 Query Match 1.4%; Score 9; DB 1; Length 826;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 635 IDKIEFIPV 643
 Db 674 IDKIEFIPV 682
 RESULT 13
 ID C9CA_BACTO STANDARD; PRT; 1157 AA.
 AC 045733;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cry9Ca (Insecticidal delta-endotoxin
DE cry9Ca(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
protein).
GN CRY9CA OR CRY9CA(A).
OS *Bacillus thuringiensis* (subsp. *tolworthi*).
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1442;
RN NCBI_TaxID=1442;
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-BT502618A;
RX MEDLINE=96141404; PubMed=8572715;
RA Lambert B., Buysse L., Decock C., Jansens S., Piens C., Saey B.,
Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peteroen M.:
RT "A *Bacillus thuringiensis* insecticidal crystal protein with a high
RT activity against members of the family Noctuidae."
RL Appl. Environ. Microbiol. 62:80-86(1996).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
CC PLOTELIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
CC BEETLE.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z37527; CAAB5764.1; -
CC DR HSSP: P07130; IDLC.
CC DR InterPro: IPR001178; Endotoxin.
CC DR Pfam: PF00555; endotoxin; 1.
CC KW Toxin; Sporulation.
CC SQ SEQUENCE 1157 AA; 129775 MW; C364391EF7EDB8A CRC64;
Query Match 1.4%; Score 9; DB 1; Length 1157;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 509 ITOLPLVKA 517
DB 515 ITOLPLVKA 523
RESULT 14
CHAA_CLOBI STANDARD; PRT; 618 AA.
ID CHAA_CLOBI
AC 005102;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal-like protein cry17Aa (insecticidal toxin
DE CRYXVIIAa) (cbm72 mosquitoicidal toxin).
GN CRY17AA OR CRYXVIIA(A) OR CBM72.
OS Clostridium bifermentans.
OC Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1490;
RN NCBI_TaxID=1490;
RP SEQUENCE FROM N.A.
RC STRAIN-CH18 / subsp. *Malaysia*;
RX MEDLINE=98267211; PubMed=9602158;
RA Barloy F., Decadet M.-M., Delecluse A.;

RT "Cloning and sequencing of three new putative toxin genes from
RT Clostridium bifermentans CH18."
RL Gene 211:293-299(1998).
CC -1- FUNCTION: NOT SIGNIFICANTLY TOXIC TO MOSQUITO LARVAE MAY INCREASE
CC THE TOXICITY OF THE PESTICIDAL CRYSTAL-LIKE PROTEIN CRY16Aa
CC (CBM71).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DEVELOPMENTAL STAGE: PRODUCED DURING SPOULATION.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X99478; CAAB6784.1; -
CC DR InterPro: IPR001178; Endotoxin.
CC DR Pfam: PF00555; endotoxin; 1.
CC KW Toxin; Sporulation.
CC FT DOMAIN 174 179 POLY-LEU.
CC SQ SEQUENCE 618 AA; 71651 MW; 1B9C5251B9AD329D CRC64;
Query Match 1.2%; Score 8; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 635 IDKIEFIP 642
DB 609 IDKIEFIP 616
RESULT 15
CTAA_BACTU STANDARD; PRT; 1138 AA.
ID CTAA_BACTU
AC 003749;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cry7Aa (insecticidal delta-endotoxin
DE CRYVIIAa) (Crystalline entomocidal protoxin) (129 kDa crystal
DE protein).
GN CRY7AA OR CRYVIIA(A) OR CRYIIIC.
OS *Bacillus thuringiensis*.
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1428;
RN NCBI_TaxID=1428;
RP SEQUENCE FROM N.A.
RX MEDLINE=92384571; PubMed=1514800;
RA Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peteroen M.:
RT "Novel *Bacillus thuringiensis* insecticidal crystal protein with a
RT silent activity against coleopteran larvae."
RL Appl. Environ. Microbiol. 58:2536-2542(1992).
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS
CC NATURAL FORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE
CC AFTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

CC -----
DR EMBL; M64478; AAA22351.1; -;
DR EMBL; A07236; CAA00646.1; -;
DR HSSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;

Query Match 1.2%; Score 8; DB 1; Length 1138;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 451 DSIDQLPP 458
|||||||
Db 438 DSIDQLPP 445

Search completed: January 10, 2003, 11:09:50
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 11:08:09 : Search time 37 Seconds
(without alignments)
3586.334 Million cell updates/sec

Title: US-09-943-692-2

Peflect score: 644
Sequence: 1 MNPNNRSEHDITKTENNENY.....TGLSAGDKYIDKIEFIPVN 644

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL_21:
1: sp._archaea:
2: sp._bacteria:
3: sp._fungi:
4: sp._human:
5: sp._invertebrate:
6: sp._mammal:
7: sp._mhc:
8: sp._organelle:
9: sp._phage:
10: sp._plant:
11: sp._rodent:
12: sp._virus:
13: sp._vertebrate:
14: sp._unclassified:
15: sp._virus:
16: sp._bacteriophage:
17: sp._archaeo:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	652	2	Q9S6N9
2	50	7.8	652	2	P81518
3	10	1.6	645	2	Q9S603
4	10	1.6	660	2	Q8R066
5	10	1.6	666	2	Q8VW62
6	9	1.4	239	2	Q86287
7	9	1.4	638	2	Q87654
8	9	1.4	719	2	Q9F0P8
9	9	1.4	1254	2	Q8VU00
10	8	1.2	138	5	Q9N6W1
11	8	1.2	260	16	Q50779
12	8	1.2	294	17	Q91P03
13	8	1.2	326	17	Q97C11
14	8	1.2	329	16	Q97D92
15	8	1.2	357	16	Q8YV71
16	8	1.2	375	16	Q9RX57

17	8	1.2	483	16	Q9S242	Q9S242 streptomyces
18	8	1.2	485	2	Q8V048	Q8V048 escherichia
19	8	1.2	555	2	Q9P03	Q9P03 rhizobium e
20	8	1.2	753	5	Q9V120	Q9V120 drosophila
21	8	1.2	760	5	Q22235	Q22235 caenorhabditis
22	8	1.2	798	5	Q9V1Y9	Q9V1Y9 drosophila
23	8	1.2	1144	2	Q45745	Q45745 bacillus th
24	8	1.2	1270	2	Q8VU01	Q8VU01 bacillus th
25	8	1.2	1420	5	Q9NFW7	Q9NFW7 drosophila
26	8	1.2	1905	3	Q92225	Q92225 emericella
27	8	1.2	3729	2	Q33956	Q33956 streptomyces
28	7	1.1	57	16	Q8X9U7	Q8X9U7 escherichia
29	7	1.1	72	5	Q61997	Q61997 bruglia paha
30	7	1.1	85	2	Q51815	Q51815 bacillus su
31	7	1.1	89	16	Q92EC3	Q92EC3 listeria in
32	7	1.1	114	17	Q96Y21	Q96Y21 sulfolobus
33	7	1.1	130	11	Q9DC39	Q9DC39 mus musculus
34	7	1.1	133	4	Q9NSM7	Q9NSM7 homo sapien
35	7	1.1	137	11	Q9E0N1	Q9E0N1 mus musculus
36	7	1.1	140	16	Q82B66	Q82B66 listeria in
37	7	1.1	140	16	Q8V6P1	Q8V6P1 listeria in
38	7	1.1	144	4	Q96J55	Q96J55 homo sapien
39	7	1.1	153	11	Q8VEQ3	Q8VEQ3 mus musculus
40	7	1.1	162	16	Q9X812	Q9X812 streptomyces
41	7	1.1	163	16	Q910V9	Q910V9 streptomyces
42	7	1.1	169	4	Q9Y6E5	Q9Y6E5 homo sapien
43	7	1.1	194	16	Q8ZAE8	Q8ZAE8 yersinia pe
44	7	1.1	196	5	Q9VG7	Q9VG7 drosophila
45	7	1.1	201	11	Q9E0N0	Q9E0N0 mus musculus

ALIGNMENTS

RESULT 1

Q9S6N9 ID Q9S6N9 PRELIMINARY; PRT; 652 AA.
AC Q9S6N9; 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-JUN-2001 (TREMURel. 17, Last annotation update)
DE Cry3Aa protein.
GN CRY3AA.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BT22;
RA Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;
RT "A novel cry3Aa gene."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ237900; CAB41411.1; -.
DR HSSP; P07130; IDC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 652 AA; 74035 MW; 544AE16E1DFF7647 CRC64;

Query Match 100.0%; Score 644; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPNNRSEHDITKTENNENYPTNHQYPLAETPNPTLEDLNYKEFLRMVADNNTAALDSS 60
Db 9 MNPNNRSEHDITKTENNENYPTNHQYPLAETPNPTLEDLNYKEFLRMVADNNTAALDSS 68
QY 61 TTKDVIQKISVVGDLGVGPFPGALVSTYTNPLNTINISSEDPKRAFMQVQALMDOK 120
Db 69 TTKDVIQKISVVGDLGVGPFPGALVSTYTNPLNTINISSEDPKRAFMQVQALMDOK 128
QY 121 INDYAKNKLAELQGNVVEDYVALSSWQKNPVSSNPHSGRIRLRFQASHRFNS 180
Db 121 INDYAKNKLAELQGNVVEDYVALSSWQKNPVSSNPHSGRIRLRFQASHRFNS 180

Db 129 IADYAKKALAELOGIONNEDVVSALSSWOKNPVSSRNPHSOGIRIELFSQAEHFRRS 188
 QY 181 MPFAISGEYEVFLTTYAQAANTHFLFKDAOYGEWGEKEDIAEFKROLKLTQET 240
 Db 189 MPFAISGEYEVFLTTYAQAANTHFLFKDAOYGEWGEKEDIAEFKROLKLTQET 248
 QY 241 DHCKKYNVGLDKRGSSYSWVNFNRRREMTLVLDLALFPLVDVRLYKREKTELT 300
 Db 249 DHCKKYNVGLDKRGSSYSWVNFNRRREMTLVLDLALFPLVDVRLYKREKTELT 308
 QY 301 RDVLDPYGVNLRGCTFFSNIENYIKRPHFDVLIQHTFRQGYGNDSPNTWS 360
 Db 309 RDVLDPYGVNLRGCTFFSNIENYIKRPHFDVLIQHTFRQGYGNDSPNTWS 368
 QY 361 GNVSTRPSIGSNDITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVPSAVYSGVT 420
 Db 369 GNVSTRPSIGSNDITSPFYGNKSEPVQNLFEENGKRYRAVANTNLAVPSAVYSGVT 428
 QY 421 KVEFSYNDQDEASTQYDTSKRNCAVSWDSIDQLPEPTTDEPLEKGYSHQLNVMCFL 480
 Db 429 KVEFSYNDQDEASTQYDTSKRNCAVSWDSIDQLPEPTTDEPLEKGYSHQLNVMCFL 488
 QY 481 MOGSRCITPVLWTNHSVDFFNMIDSKITQLPLVKAVALSGASVAVGPRFTGGDIQC 540
 Db 489 MOGSRCITPVLWTNHSVDFFNMIDSKITQLPLVKAVALSGASVAVGPRFTGGDIQC 548
 QY 541 TENGSAATYTPDVSYSKYRARIHYASTQITFTLSLDGAPNQYFEDKTKNGDTLT 600
 Db 549 TENGSAATYTPDVSYSKYRARIHYASTQITFTLSLDGAPNQYFEDKTKNGDTLT 608
 QY 601 YNSFNLASFPPELSSGNLQIGVGLSAGDKVYIDKEEIPVN 644
 Db 609 YNSFNLASFPPELSSGNLQIGVGLSAGDKVYIDKEEIPVN 652

RESULT 2

PRELIMINARY; PRT; 50 AA.
 ID P81518
 AC P81518;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE 70 kDa CRYSTAL protein (Delta endotoxin) (CRYSTALLINE ENTOMOCIDAL DE PROTOXIN) (Fragment).
 GN CRYTIIA.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 CC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE OF 1-50 FROM N.A.
 RC STRAIN-LM79;
 RA MEDLINE-9325939; PubMed-8491716;
 RX de Souza M., Lecadet M.M., Lerecuis D.;
 RT "Full expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a distant upstream DNA sequence affecting transcription.";
 RL J. Bacteriol. 175:2952-2960(1993).
 CC -1- FUNCTION: PROMOTES COLLOIDSMORPHIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLEOPTERA.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
 DR EMBL: L03393; AAA22350.1; -;
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 KW Toxin; Sporulation.
 FT NON_TER 50
 SQ SEQUENCE 50 AA; 5829 MW; 9AALFD4DFCE7B808 CRC64;

Query Match

Best Local Similarity 7.8%; Score 50; DB 2; Length 50;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNRSEHDTIKTTENNNEVPTNHVQYPLAEFPNPTLEDLANKKEFLRMWA 50

Db 1 MNPNNRSEHDTIKTTENNNEVPTNHVQYPLAEFPNPTLEDLANKKEFLRMWA 50

RESULT 3

PRELIMINARY; PRT; 645 AA.
 ID 09S603
 AC 09S603;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Delta-endotoxin (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 CC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROVAR JAPONENSIS TYPE.
 RX MEDLINE-99025985; PubMed-9806979;
 RA Masano N., Ohda M.;
 RT Assignment of delta-endotoxin genes of the four lepidoptera-specific Bacillus thuringiensis strains that produce spherical parasporal inclusions.";
 RT Curr. Microbiol. 37:408-411(1998).
 DR EMBL: AF042733; AAB97923.1; -;
 DR HSP: P07130; IDIC.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin.1.
 FT NON_TER 1
 SQ SEQUENCE 645 AA; 72967 MW; 143E51312B890CE3 CRC64;

Query Match 1.6%; Score 10; DB 2; Length 645;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 ITQPLVAVAY 518
 Db 516 ITQPLVAVAY 525

RESULT 4

PRELIMINARY; PRT; 660 AA.
 ID 08R006
 AC 08R006;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Insecticidal crystal protein bun2 (Fragment).
 GN CRYBUN2.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 CC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ito T., Sahara K., Bando H.;
 RT Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawa Encoding a Mosquitocidal Proteins.";
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB074413; BAB72016.2; -;
 FT NON_TER 1
 SQ SEQUENCE 660 AA; 75643 MW; A92FE6257C2B9404 CRC64;

Query Match 1.6%; Score 10; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 VYDKIEFIP 642
 Db 624 VYDKIEFIP 633

RESULT 5

Q8VM62 PRELIMINARY: PRT: 666 AA.

AC Q8VM62:

DT 01-MAR-2002 (TREMBLREL. 20, Created)

DT 01-MAR-2002 (TREMBLREL. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLREL. 21, Last annotation update)

DE Insecticidal crystal protein buns3 (Fragment).

GN CRYBUN3.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA Ito T., Sahara K., Asano S., Bando H.;

RT "Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins.";

RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL: AB074414; BAF72018.1; -

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 666 AA; 75311 MW; A87853FAE8FAA1D CRC64;

Query Match 1.6%; Score 10; DB 2; Length 666;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 269 RREMTLVLD 278

Db 280 RREMTLVLD 289

RESULT 6

Q86287 PRELIMINARY: PRT: 239 AA.

AC Q86287:

DT 01-NOV-1998 (TREMBLREL. 08, Created)

DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)

DT 01-JUN-2002 (TREMBLREL. 21, Last annotation update)

DE Hypothetical 27.6 kDa protein.

GN ORC.

OS Lactococcus lactis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Lactococcus.

OX NCBI_TaxID=1358;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-N8; TRANSPOSON-TN5481;

RT MEDLINE-94452384; PubMed-10524753;

RA Immonen T., Wahlstrom G., Takala T., Saris P.E.J.;

RT "Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis N8.";

RT DNA Seq. 9:245-261(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN-N8; TRANSPOSON-TN5481;

RT MEDLINE-94452385; PubMed-10524754;

RA Immonen T., Saris P.E.J.;

RT "Characterization of the nlsFEG operon of the nlsin 2 producing Lactococcus lactis subsp. lactis N8 strain.";

RT DNA Seq. 9:263-274(1998).

DR EMBL: AJ000993; CA04444.1; -

DR InterPro: IPR000160; GGDEF.

DR Pfam: PF00990; GGDEF. 1.

DR SMART: SM00267; DUF1. 1.

DR TIGRFA: TIGR00254; GGDEF. 1.

KW Hypothetical protein; Plasmid.

SQ SEQUENCE 239 AA; 27630 MW; 96E3258044D23FD CRC64;

Query Match 1.4%; Score 9; DB 2; Length 239;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 320 TFSNIENYI 328

Db 209 TFSNIENYI 217

RESULT 7

Q87654 PRELIMINARY: PRT: 638 AA.

AC Q87654:

DT 01-NOV-1998 (TREMBLREL. 08, Created)

DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)

DE Delta-endotoxin (Fragment).

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-92-KU-149-8;

RT MEDLINE-21064760; PubMed-11136135;

RA Wasano N., Ohda M., Miyamoto K.;

RT "Two delta-Endotoxin Genes, cry9Da and a Novel Related Gene, Commonly Occurring in Lepidoptera-Specific Bacillus thuringiensis Japanese Isolates that Produce Spherical Parasporal Inclusions.";

RT Curr. Microbiol. 42:129-133(2001).

RL EMBL: AF093107; AAC63366.1; -

DR HSSP: P07130; IDLC.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

FT NON_TER 1

SQ SEQUENCE 638 AA; 71993 MW; 1817831FEF080A61 CRC64;

Query Match 1.4%; Score 9; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 509 ITQLPLVKA 517

Db 509 ITQLPLVKA 517

RESULT 8

Q9F0P8 PRELIMINARY: PRT: 719 AA.

AC Q9F0P8:

DT 01-MAR-2001 (TREMBLREL. 16, Created)

DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)

DE Cry11.

GN Cry11.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-BTC007;

RT "The cloning of a novel cry11 gene from Bacillus thuringiensis strain.";

RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF211190; AA643526.1; -

DR HSSP: P02965; IC1Y.

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

KW Plasmid.

SO SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match 1.4%; Score 9; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 276 VLDIALFP 284

DB 268 VLDIALFP 276

RESULT 9

08VUL0

AC 08VUL0 PRELIMINARY; PRT; 1254 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

GN CRYE60.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA Takebe S., Matsumura T., Izumoto Y., Komano T.;

RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB075461; BAB78602.1; -

DR InterPro: IPR001178; Endotoxin.

DR Pfam: PF00555; endotoxin; 1.

SO SEQUENCE 1254 AA; 142554 MW; BD35AB7653CF12DC CRC64;

Query Match 1.4%; Score 9; DB 2; Length 1254;

Best Local Similarity 100.0%; Pred. No. 6.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 635 IKKIEPIV 643

DB 657 IKKIEPIV 665

RESULT 10

09N6M1

AC 09N6M1 PRELIMINARY; PRT; 138 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE Mod(mdg4)54.6 (Fragment).

GN MOD(mdg4) OR CG7836 OR CG8076 OR CG15802.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20253099; PubMed=10790390;

RA Buechner K., Roth P., Schotta G., Krauss V., Saumweber H., Reuter G.,

RA Dorn R.;

RT "Genetic and molecular complexity of the position effect variegation

RT Genetics 155:141-157(2000)."

RL EMBL; AJ277178; CAB85473.1; -

DR FlyBase; FBgn0002781; mod(mdg4).

FT NON_TER

SO SEQUENCE 138 AA; 15414 MW; F8326FED6FC2C42 CRC64;

Query Match 1.2%; Score 8; DB 5; Length 138;

Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 302 DVLTDPV 309

DB 46 DVLTDPV 53

RESULT 11

050779

AC 050779 PRELIMINARY; PRT; 260 AA.

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical protein BBJ24.

GN BBJ24.

OS Borrelia burgdorferi (Lyme disease spirochete).

OG Plasmid lp38.

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI_TaxID=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35210 / B31;

RX MEDLINE=98065943; PubMed=9403685;

RA Fraser C.M., Castens S., Huang W.M., Sutton G.G., Clayton R.A.,

RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

RA Peterson J., Kervatage A.R., Quackenbush J., Salzberg S., Hanson M.,

RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

RA Ullrich S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

RA Smith H.O., Venter J.C.;

RT "Genomic sequence of a Lyme disease spirochete, Borrelia

RT burgdorferi."

RL Nature 390:580-586(1997).

DR EMBL; AE000787; AAC66120.1; -

DR TIGR; BBJ24;

KW Hypothetical protein; Plasmid; Complete proteome.

SO SEQUENCE 260 AA; 30484 MW; B0102AF885DCBE CRC64;

Query Match 1.2%; Score 8; DB 16; Length 260;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 632 KYIDKIE 639

DB 22 KYIDKIE 29

RESULT 12

091FD3

AC 091FD3 PRELIMINARY; PRT; 294 AA.

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

GN 391R.

OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).

OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.

OX NCBI_TaxID=10488;

RN [1]

RP SEQUENCE FROM N.A.

RA Deltis H., Darai G., Fluegel R.M.;

RT "DNA analysis of insect iridescent virus 6: evidence for circular

RT permutation and terminal redundancy."

RL J. Virol. 49:609-614(1984).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86174607; PubMed=3959991;

RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;

RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis

RT in mice."

RL Med. Microbiol. Immunol. 175:43-53(1986).
 RP SEQUENCE FROM N.A.
 RA MEDLINE-87321126; PubMed-2820141;
 RA Schiltzler P., Soltan J.B., Fischer M., Relenser H., Scholz J.,
 RA Delius H., Darai G.;
 RT "Molecular cloning and physical mapping of the genome of insect
 RT iridescent virus type 6: further evidence for circular permutation of
 RT the viral genome.";
 RL Virology 160:66-74(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-89073752; PubMed-3201750;
 RA Fischer M., Schiltzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in
 RT the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-92196996; PubMed-1549908;
 RA Handermann M., Schiltzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
 RA Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93118242; PubMed-1475907;
 RA Sonntag K.C., Darai G.;
 RT "Characterization of the third origin of DNA replication of the genome
 RT of insect iridescent virus type 6.";
 RL Virus Genes 6:333-342(1992).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93260401; PubMed-8492091;
 RA Stohwasser R., Raab K., Schiltzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 RT insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94167241; PubMed-8121799;
 RA Schiltzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
 RT in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 RN [9]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94353641; PubMed-8073636;
 RA Sonntag K.C., Schiltzler P., Koonin E.V., Darai G.;
 RT "Chilo iridescent virus encodes a putative helicase belonging to a
 RT distinct family within the 'Dead/H' superfamily: implications for the
 RT evolution of large DNA viruses.";
 RL Virus Genes 8:151-158(1994).
 RN [10]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-95213160; PubMed-7698884;
 RA Sonntag K.C., Schiltzler P., Janssen W., Darai G.;
 RT "Identification of the primary structure and the coding capacity of
 RT the genome of insect iridescent virus type 6 between the genome
 RT coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
 RN [11]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94282906; PubMed-8021587;
 RA Schiltzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
 RA Koonin E.V., Darai G.;
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the
 RT largest subunit of eukaryotic RNA polymerase II.";
 RL J. Gen. Virol. 75:1557-1567(1994).
 RN [12]

RP SEQUENCE FROM N.A.
 RA MEDLINE-98141693; PubMed-9482589;
 RA Bahr U., Tildona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome
 RT coordinates 0.101 and 0.391: similarities in coding strategy between
 RT insect and vertebrate iridoviruses.";
 RL Virus Genes 15:235-245(1997).
 RN [13]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99125223; PubMed-9926400;
 RA Muller K., Tildona C.A., Bahr U., Darai G.;
 RT "Identification of a thymidylate synthase gene within the genome of
 RT Chilo iridescent virus.";
 RL Virus Genes 17:243-258(1998).
 RN [14]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99383793; PubMed-10456793;
 RA Muller K., Tildona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 RT iridescent virus encoding enzymes involved in viral DNA replication
 RT and processing.";
 RL Virus Genes 18:243-264(1999).
 RN [15]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-21342589; PubMed-11448171;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the First Complete DNA Sequence of an Invertebrate
 RT Iridovirus: Coding Strategy of the Genome of Chilo iridescent Virus.";
 RL Virology 286:182-196(2001).
 RN [16]
 RP SEQUENCE FROM N.A.
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF303741; AAK82251.1; -
 DR InterPro: IPR000822; Znf C2H2.
 DR Pfam: PF00096; Zf-C2H2; 1.
 KW DNA-binding; Zinc-finger.
 SQ SEQUENCE 294 AA; 34614 MW; 761C8CE489CE86D CRC64;
 Query Match 1.2%; Score 8; DB 12; Length 294;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 462 DEPLEXY 469
 DB 68 DEPLEXY 75
 RESULT 13
 Q97C11
 ID Q97C11 PRELIMINARY; PRT; 326 AA.
 AC Q97C11;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Hypothetical protein TV0294.
 DE TV0294 OR TVG0304564.
 GN Thermoplasma volcanium.
 OS Thermoplasma volcanium.
 OC Archaea: Euryarchaeota: Thermoplasmata: Thermoplasmatales;
 CC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GSSI / DSM 4299 / JCM 9571;
 RX MEDLINE-20570466; PubMed-11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Aramaki H., Makino K., Kaneshiro K.,
 RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 RT sequence of Thermoplasma volcanium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL: AP000992; BAB59436.1; -
 DR InterPro: IPR001387; HTH_3.

DR Pfam; PF01381; HTH_3; 1.
 DR SMART; SM00530; HTH_XRE; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 326 AA; 36773 MW; D10685EEEC08C931 CRC64;

Query Match 1.2%; Score 8; DB 17; Length 326;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 ENGSAATI 549
 |||||
 DB 176 ENGSAATI 183

RESULT 14
 O97D92 PRELIMINARY; PRT; 329 AA.

AC O97D92.
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE DNA replication protein DnaC.
 GN CAC3588.
 OS Clostridium acetobutylicum.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 CC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE-21359325; PubMed-11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
 RA Tatusev R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007855; AAK81511.1; -.
 KW Complete proteome.
 SQ SEQUENCE 329 AA; 36693 MW; 91578425D5C2958E CRC64;

Query Match 1.2%; Score 8; DB 16; Length 329;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 PNPTLEDL 40
 |||||
 DB 235 PNPTLEDL 242

RESULT 15
 O8YVRI

ID O8YVRI PRELIMINARY; PRT; 357 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 6-phosphofructokinase.
 GN ALR1913.
 OS Anabaena sp. (strain PCC 7120).
 CC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21595285; PubMed-11759840;
 RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iritani M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120";

RL DNA Res. 8:205-213(2001).
 DR EMBL; AF003587; BAB73612.1; -.
 DR InterPro; IPR000023; PpfFructKinase.
 DR Pfam; PF00365; Pfk_1
 DR PRINTS; PR00476; PFERCTKINASE.
 DR ProDom; PD000707; PpfFructKinase; 1.
 DR PROSITE; PS00433; PHOSPHOFRICTOKINASE; 1.
 KW Kinase; Complete proteome.
 SQ SEQUENCE 357 AA; 38006 MW; 40A6C3C266A6E5D0 CRC64;

Query Match 1.2%; Score 8; DB 16; Length 357;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 592 TINKGDTL 599
 |||||
 DB 77 TINKGDTL 84

Search completed: January 10, 2003, 11:10:35
 Job time : 39 secs